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HUMAN xiap

SEQ ID NO:3	1	gaaaagggtggacaagtcctaat	60
		ttcaagagaagatgacttttaacag	
		tttgaaggatct	
SEQ ID NO:4 a		M T F N S F E G S	-
	61	aaaactgtgtacctgcagacatcaataaggaaga	120
		aatgttagaagagtttaataaga	
		K T C V P A D I N K E E F V E F N R	-
	121	ttaaaaacttttgctaattttccaagtgtagtcctg	180
		tttcagcatcaacactggcacga	
		L K T F A N F P S G S P V S A S T L A R	-
	181	gcagggttcttatactggtgaaggagataccgtgcggt	240
		ctttagttgtcatgcagct	
		A G F L Y T G E G D T V R C F S C H A A	-
	241	gtagatagtggaatatggagactcagcagttggaagacacaggaag	300
		atcccccaat	
		V D R W Q Y G D S A V G R H R K V S P N	-
	301	tgcagatttatcaacggcttttatcttgaaaatagtgccacgcagtc	360
		tacaaaattctggt	
		C R F I N G F Y L E N S A T Q S T N S G	-

Fig. 1 (page 1 of 7)

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HUMAN xiap

```
361 atccagaatggtcagtacaaagttgaaactatctgggaagcagagatcatttgcctta 420
-----+-----+-----+-----+-----+-----+
a I Q N G Q Y K V E N Y L G S R D H F A L -
421 gacaggcatctgagacacatgcagactatctttgagaactgggcagggttagatata 480
-----+-----+-----+-----+-----+-----+
a D R P S E T H A D Y L L R T G Q V V D I -
481 tcagacaccatatacccgaggaaacctgccatgtattgtgaagaagctagattaaagtcc 540
-----+-----+-----+-----+-----+-----+
a S D T I Y P R N P A M Y C E E A R L K S -
541 tttcagaactggccagactatgctcacctaaccccaagagagtagcaagtgctggactc 600
-----+-----+-----+-----+-----+-----+
a F Q N W P D Y A H L T P R E L A S A G L -
601 tactacacaggtaattggtgaccaagtgcagtgcttttgtgtggtggaactgaaaaat 660
-----+-----+-----+-----+-----+-----+
a Y Y T G I G D Q V Q C F C C G G K L K N -
661 tgggaaccttgatcgatcgctggtcagaacacagcgacactttcctaattgctcttt 720
-----+-----+-----+-----+-----+-----+
a W E P C D R A W S E H R R H F P N C F F -
```

Fig. 1 (page 2 of 7)

HUMAN xiap

721	gttttgggccaatcttaatatcgaagtgaatctgatgctgtgagttctgataggaat	780
a	V L G R N L N I R S E S D A V S S D R N	-
781	ttcccaaatccaacaatctccaagaatcccatggcagattatgaagcacggatc	840
a	F P N S T N L P R N P S M A D Y E A R I	-
841	tttacttttgggacatggatatactcagttaacaaggagcagcttgcaagagctggattt	900
a	F T F G T W I Y S V N K E Q L A R A G F	-
901	tatgctttaggtgaagtgataaagtgtcttccactgtggaggaggctaaactgat	960
a	Y A L G E G D K V K C F H C G G G L T D	-
961	tggaagcccagtgaaagacccttggaacaacatgctaaatgggtatccagggtgcaaatat	1020
a	W K P S E D P W E Q H A K W Y P G C K Y	-
1021	ctgttagaacagaaggacaagaatatataaacaatatcttaactcattcacttgag	1080
a	L L E Q K G Q E Y I N N I H L T H S L E	-

Fig. 1 (page 3 of 7)

1081	gagtgctcgtggaactactgagaaaacaccatcactaactagaagaattgatgatacc	1140
a	E C L V R T T E K T P S L T R R I D D T	-
1141	atcttccaaaatcctatggtacaagaagctatacgaatggggttcagtttcaaggacatt	1200
a	I F Q N P M V Q E A I R M G F S F K D I	-
1201	aagaaaataatggaggaaaaattcagatatctgggagcaactataaatcacttgaggtt	1260
a	K K I M E E K I Q I S G S N Y K S L E V	-
1261	ctggttcagatctagtgaatgctcagaagacagtatgcaagatgagtcgaagtcagact	1320
a	L V A D L V N A Q K D S M Q D E S S Q T	-
1321	tcattacagaagagattagtactgaagagcagctaaggcgctgcaagaggagaagctt	1380
a	S L Q K E I S T E E Q L R R L Q E E K L	-
1381	tgcaaaaatctgtatggatagaaaattgctatcgtttttgttccttgtggacatctagtc	1440

Fig. 1 (page 4 of 7)

HUMAN xiap

a	C	K	I	C	M	D	R	N	I	A	I	V	F	V	P	C	G	H	L	V	-
1441	acttgtaacaatgtgctgaagcagttgacaagtg	ccccatgtgctacacagtcattact	-----+-----+ 1500																		
a	T	C	K	Q	C	A	E	A	V	D	K	C	P	M	C	Y	T	V	I	T	-
1501	ttcaagcaaaaattttatgtcttaactctata	taggcatgttatgtgttctt	-----+-----+ 1560																		
a	F	K	Q	K	I	F	M	S	*											-	
1561	tattaccctgattgaatgtgtgatgtgaactg	actttaagtaatcaggattgaattccat	-----+-----+ 1620																		
a																				-	
1621	tagcatttgctaccaagtaggaaaaaatgtac	atggcagtgtttagttggcaatata	-----+-----+ 1680																		
a																				-	
1681	atccttgaaatttcttgatttttcagggtat	tagctgtattatccatttttttactgtta	-----+-----+ 1740																		
a																				-	
1741	tttaattgaaaccatagactaagaataaga	agcatcatactataactgaacacaatgtgt	-----+-----+ 1800																		
a																				-	

Fig. 1 (page 5 of 7)

[illegible]

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HUMAN xiap

a	2161	nagatatgttaagtgtaaaatgcaagtggcnnnnacactatgtatagtctgagccagatca	2220
		-	
	2221	aagtatgtatgttnttaatatgcatagaacnanagatttggaagatatatacccaaactg	2280
		-	
a	2281	ttaaatgtggtttctcttcggggagggggatgggggagggggccagaggggttta	2340
		-	
a	2341	naggggccttttcactttcnacttttttcattttgttctgttcgnattttttataagtat	2400
		-	
a	2401	gtanaccnnaagggttttatggnaactaacaatcagtaacctaaaccccgtagctatcct	2460
		-	
a	2461	gtnccttcctaggagctgtnttgtttcccaccaccaccttccctctgaacaaatgc	2520
		-	
a	2521	ctgagtgtctggggcactttn	2540
		-	
a			

Fig. 1 (page 7 of 7)

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SEQ ID NO:5
1 TCCTTGAGATGATCAGTATAGGATTAGGATCTCCATGTTGGAACCTCTAAATGCATAGA
-----+-----+-----+-----+-----+-----+ 60
C -
61 AATGGAAATAATGGAAATTTTTCATTTTGGCTTTTCAGCCTAGTATTAAACTGATAAAA
-----+-----+-----+-----+-----+-----+ 120
C -
121 GCAAAGCCATGCACAAACTACCTCCCTAGAGAAAGGCTAGTCCCTTTTCTTCCCATTC
-----+-----+-----+-----+-----+-----+ 180
C -
181 ATTCATTATGAACATAGTAAACAGCATATTCTTATCAAAATTGATGAAAGCGCCA
-----+-----+-----+-----+-----+-----+ 240
SEQ ID NO:6 C M N I V E N S I F L S N L M K S A N -
241 ACACGTTTGAAC TGAATACGACTTGTCATGTGAACTGTACCGAATGTCTACGTATTCCA
-----+-----+-----+-----+-----+-----+ 300
C T F E L K Y D L S C E L Y R M S T Y S T -
301 CTTTCCCTGCTGGGTTCCCTGCTCAGAAAGGAGTCTTGCTCGTGGTTTCTATTACA
-----+-----+-----+-----+-----+-----+ 360
C F P A G V P V S E R S L A R A G F Y Y T -

Fig. 2 (page 1 of 8)

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HUMAN hiap-1

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361      CTGGTGTGAATGACAAGGTCAAATGCTTCTGTGTGGCCTGATGCTGGATAACTGGAAAA 420
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      G V N D K V K C C F C C G L M L D N W K R -

421      GAGGAGACAGTCCTACTGAAAGCATAAAAGTTGTATCCTAGCTGCAGATTCGTTTCAGA 480
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      G D S P T E K H K K L Y P S C R F V Q S -

481      GTCTAAATTCCGTTAACTTGGAAGCTACCTCTCAGCCTACTTTTCTCTTCTTCAGTAA 540
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      L N S V N N L E A T S Q P T F P S S V T -

541      CACATCCACACTCATTAATTCGGGTACAGAAACAGTGGATATTTCCGTGGCTCTT 600
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      H S T H S L L P G T E N S G Y F R G S Y -

601      ATTCAAACTCTCCATCAAATCCTGTAACTCCAGAGCAAATCAAGAATTTCTGCCTTGA 660
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      S N S P S N P V N S R A N Q E F S A L M -

661      TGAGAAGTTCCTACCCCTGTCCAATGAATAACGAAATGCCAGATTACTTTTCAGA 720
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      R S S Y P C P M N N E N A R L L T F Q T -
```

Fig. 2 (page 2 of 8)

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HUMAN hiap-1

```

721 CATGGCCATTGACTTTTCTGTCGCCAACAGATCTGGCAGCAGCAGGCTTTTACTACATAG 780
-----+-----+-----+-----+-----+-----+-----+
C      W P L T F L S P T D L A R A G F Y Y I G -

781 GACCTGGAGACAGAGTGGCTTGCTTTGCTGTGCTGGTGGAAATTGAGCAATTGGGAACCGA 840
-----+-----+-----+-----+-----+-----+-----+
C      P G D R V A C F A C G G K L S N W E P K -

841 AGGATAATGCTATGTCAGAACACCTGAGACATTTCCCAAATGCCCATTTATAGAAAATC 900
-----+-----+-----+-----+-----+-----+-----+
C      D N A M S E H L R H F P K C P F I E N Q -

901 AGCTTCAAGACACTTCAAGATACACAGTTTCTAATCTGAGCATGCAGACATGCAGCCC 960
-----+-----+-----+-----+-----+-----+-----+
C      L Q D T S R Y T V S N L S M Q T H A A R -

961 GCTTTAAACATTCTTTAACTGGCCCTCTAGTGTTCTAGTTAATCCTGAGCAGCTTGCAA 1020
-----+-----+-----+-----+-----+-----+-----+
C      F K T F F N W P S S V L V N P E Q L A S -

1021 GTGCGGGTTTATTATGTGGTAACAGTGATGATGTCAAATGCTTTTGTGTGATGGTG 1080
-----+-----+-----+-----+-----+-----+-----+
C      A G F Y Y V G N S D D V K C F C C D G G -
```

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HUMAN hiap-1

```
1081 GACTCAGGTGTTGGGAATCTGGAGATGATCCATGGTTCAACATGCCAAGTGGTTTCCAA 1140
      L R C W E S G D D P W V Q H A K W F P R -
1141 GGTGTGAGTACTTGATAAGAATTAAAGACAGGAGTTTCATCCGTCAAGTTCAAGCCAGTT 1200
      C E Y L I R I K G Q E F I R Q V Q A S Y -
1201 ACCCTCATCTACTTGAACAGCTGCTATCCACATCAGACAGCCAGGAGATGAAATGCGAG 1260
      P H L L E Q L L S T S D S P G D E N A E -
1261 AGTCATCAATTATCCATTGGAACCTGGAGAAGACCATTCAGAAGATGCAATCATGATGA 1320
      S S I I H L E P G E D H S E D A I M M N -
1321 ATACTCCTGTGATTAAATGCTGCCGTGGAAATGGGCTTTAGTAGAAGCCTGGTAAACAGA 1380
      T P V I N A A V E M G F S R S L V K Q T -
1381 CAGTTCAGAGAAAAATCCTAGCAACTGGAGAGAAATTATAGACTAGTCAATGATCTTGTGT 1440
      V Q R K I L A T G E N Y R L V N D L V L -
```

Fig. 2 (page 4 of 8)

1441	TAGACTTACTCAATGCAGAAAGATGAAATAAGGGAAGAGAGAGAGAAAGAGCAACTGAGG	1500
C	D L L N A E D E I R E E R E R A T E E -	
1501	AAAAGAATCAAATGATTATTATTATCCGGAAGAAATAGAAATGGCACTTTTCAACATT	1560
C	K E S N D L L L I R K N R M A L F Q H L -	
1561	TGACTTGTGTAATTCCAATCCTGGATAGTCTACTAACTGCCGGAATTATTAAATGAACAAG	1620
C	T C V I P I L D S L L T A G I I N E Q E -	
1621	AACATGATGTTATTAAACAGAAGACACAGACGCTTTTACAAGCAAGAGAACTGATTGATA	1680
C	H D V I K Q K T Q T S L Q A R E L I D T -	
1681	CGATTTTAGTAAAGGAAATATTGCAGCCACTGTATTCAGAAACTCTCTGCAAGAAGCTG	1740
C	I L V K G N I A A T V F R N S L Q E A E -	
1741	AAGCTGTGTATATGAGCATTTATTGTGTCAACAGCACATAAAATATATCCACAGAAG	1800
C	A V L Y E H L F V Q Q Q D I K Y I P T E D -	

Fig. 2 (page 5 of 8)

HUMAN hiap-1

1801	ATGTTTCAGATCTACCAAGTGAAGAACAAATTGCGGAGACTACCAGAAAGAAACATGTA	1860
C	V S D L P V E E Q L R R L P E E R T C K -	
1861	AAGTGTGTATGGACAAAGAAGTGTCCATAGTGTATTTCCTTGTTGGTCATCTAGTAGTAT	1920
C	V C M D K E V S I V F I P C G H L V V C -	
1921	GCAAAGATTGTGCTCCTTCTTTAAGAAAGTGTCCCTATTGTAGGAGTACAATCAAGGTA	1980
C	K D C A P S L R K C P I C R S T I K G T -	
1981	CAGTTCGTACATTCTTTCATGAAGAAGAACCAACATCGTCTAAACTTTAGAAATTAAT	2040
C	V R T F L S *	
2041	TTATTAAATGTATTATAACTTTTAACTTTTATCCTAATTGGTTCCTTAAATTTTATT	2100
C		
2101	TATTACAACCTCAAAAACATTTGTTGTGAACATATTTATATATGTATCTAAACCATA	2160
C		

Fig. 2 (page 6 of 8)

[illegible]

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HUMAN hiap-1

2521	CAGTGTCC	TATACATCGAAGGTGTCATATATGTTGAATCACA	TTTAGGACATGGTGT	2580
	- - - - -	+ + + + +	- - - - -	
				-
2581	TTTTATAA	GAAATTCTGTGAGXAAAAATTTAATAAAGCAAC	CXAAATTACTCTTAAAAAA	2640
	- - - - -	+ + + + +	- - - - -	
				-
2641	AAAAAAAA	AAAACTCGAGGGGCCCGTACCAAT		2676
	- - - - -	+ + + + +	- - - - -	
				-
				-

Fig. 2 (page 8 of 8)

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HUMAN hiap-2

SEQ ID NO:7	1	TTAGTTACCTGAAAGAGTTACTACAACCCCAAGAGTTGTGTTCTAAGTAGTATCTTGG	60
a		-	-
	61	TAATTCAGAGAGATACTCATCCTACCTGAATATAAAGTGAATAATCCAGTAAAGAAAG	120
a		-	-
	121	TGTAGTAAATTCTACATAAGAGTCTATCATTTGATTTCTTTTGTGGTGGAAATCTTAGTT	180
a		-	-
	181	CATGTGAAGAAATTTCATGTGAATGTTTGTAGTATCAAAACAGTACTGTACCTACTCATG	240
a		-	-
	241	CACAAACTGCCTCCCAAGACTTTTCCAGGTCCCTCGTATCAAAACATTAAGAGTATA	300
SEQ ID NO:8	a	H K T A S Q R L F P G P S Y Q N I K S I	-
	301	ATGGAAGATAGCACGATCTTGTTCAGATTGGACAACACAGCAACAAATAATGAAGTAT	360
a		M E D S T I L S D W T N S N K Q K M K Y	-

Fig. 3 (page 1 of 7)

HUMAN hiap-2

361	GACTTTCTGTGA	CTCTACAGAA	TGTCTACA	TATTCAA	TTTCCCCG	CGGGTG	CCT	420													
	-----+	-----+	-----+	-----+	-----+	-----+	-----+														
a	D	F	S	C	E	L	Y	R	M	S	T	Y	S	T	F	P	A	G	V	P	-
421	GTC	CAGAA	AGGAG	CTT	GTCT	CGT	CGT	GGT	TTT	TAT	TAT	ACT	GGT	GT	GAA	T	GAC	AA	GG	T	C
	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+
a	V	S	E	R	S	L	A	R	A	G	F	Y	Y	T	G	V	N	D	K	V	-
481	AA	TGCT	TCTGT	TGGC	CTG	ATG	CTGG	ATA	ACTG	GAA	ACTAG	GAC	AGT	CCT	AT	TCA	A				
	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+
a	K	C	F	C	C	G	L	M	L	D	N	W	K	L	G	D	S	P	I	Q	-
541	AAG	CATA	AAC	AGC	TAT	ATC	CTAG	CTG	TAG	CTT	TAT	TCA	GAA	TCT	GTT	CAG	CTAG	CTG			
	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+
a	K	H	K	Q	L	Y	P	S	C	S	F	I	Q	N	L	V	S	A	S	L	-
601	GG	ATCC	ACCT	CTA	AGA	ATA	CGT	CTC	CAAT	GAG	AA	CAG	TTT	GC	ACAT	TCA	TAT	CT	CCC		
	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+
a	G	S	T	S	K	N	T	S	P	M	R	N	S	F	A	H	S	L	S	P	-
661	AC	CTTG	GA	CA	TAG	CTT	GTT	CAG	TGG	TTCT	TACT	CC	AG	CC	TTCC	TCA	AA	CC	CT	CTT	
	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+	-----+
a	T	L	E	H	S	S	L	F	S	G	S	Y	S	S	L	P	P	N	P	L	-

Fig. 3 (page 2 of 7)

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721  AATCTAGAGCAGTTGAAGACATCTTCTCATCGAGGACTAACCCCTACAGTTATGCAATG 780
      N S R A V E D I S S R T N P Y S Y A M -
      AGTACTGAAGAAGCCAGATTCTTACCTACCATATGTGGCCATTAACTTTTGTGTCACCA 840
      S T E E A R F L T Y H M W P L T F L S P -
      TCAGAAATTGGCAAGAGCTGTTTATTATATAGGACCTGGAGATAGGCTGCTGCTTT 900
      S E L A R A G F Y Y I G P G D R V A C F -
      GCCTGTGGTGGGAAGCTCAGTAAGTGGAAACCAAGGATGCTATGTCAGAACACCGG 960
      A C G G K L S N W E P K D D A M S E H R -
      AGGCATTTCCCAACTGTCCATTTTGGAAAAATCTCTAGAAACTCTGAGGTTTAGCATT 1020
      R H F P N C P F L E N S L E T L R F S I -
      TCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACATTATGTACTGGCCATCT 1080
      S N L S M Q T H A A R M R T F M Y W P S -

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Fig. 3 (page 3 of 7)

HUMAN hiap-2

1081	AGTGTTCAGTTCAGCCTGAGCAGCTTGCAAGTGGTGGTTTATTATGTTGGTCGCAAT	1140
a	S V P V Q P E Q L A S A G F Y Y V G R N	-
1141	GATGATGTCAAATGCTTTGGTTGTGATGGTGGCTTGAGGTTGGGAATCTGGAGATGAT	1200
a	D D V K C F G C D G G L R C W E S G D D	-
1201	CCATGGGTAGAACATGCCAAGTGGTTTCCAAGGTGTGAGTCTTGATACGAATGAAAGGC	1260
a	P W V E H A K W F P R C E F L I R M K G	-
1261	CAAGAGTTTGTGATGAGATTCAAGGTAGATATCCTCATCTTCTTGAACAGCTGTGTGCA	1320
a	Q E F V D E I Q G R Y P H L L E Q L L S	-
1321	ACTTCAGATACCACTGGAGAAGAAATGCTGACCCACCAATTATTCATTTGGACCTGGA	1380
a	T S D T T G E E N A D P P I I H F G P G	-
1381	GAAAGTCTTCAGAAGATGCTGTCATGATGAATACACCTGTGGTTAAATCTGCCTTGGA	1440
a	E S S S E D A V M M N T P V V K S A L E	-

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1441	ATGGGCTTTAATAGAGACCTGGTGAAACAACAGTTCTAAGTAAATCCTGACAACTGGA	1500
a	M G F N R D L V K Q T V L S K I L T T G	-
1501	GAGAACTATAAACAGTTAATGATATTGTGTCAGCACTTCTTAATGCTGAAGATGAAAAA	1560
a	E N Y K T V N D I V S A L L N A E D E K	-
1561	AGAGAAGAGGAGAAGGAAAAACAAGCTGAAGAAATGGCATCAGATGATTTGTCTAATAAT	1620
a	R E E E K E K Q A E E M A S D D L S L I	-
1621	CGGAAGAACAGAAATGGCTCTCTTTCAACAATTGACATGTGTGCTTCCCTATCCTGGATAAT	1680
a	R K N R M A L F Q Q L T C V L P I L D N	-
1681	CTTTTAAAGGCCAATGTAATTAATAACAGGAACATGATATTATAACAAAAACACAG	1740
a	L L K A N V I N K Q E H D I I K Q K T Q	-
1741	ATACCTTTACAAGCGAGAGAACTGATTGATACCATTTGGGTTAAGGAAATGCTGCGGCC	1800
a	I P L Q A R E L I D T I W V K G N A A A	-

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HUMAN hiap-2

1801	AACATCTTCAAAACTGTCTAAAGAAATTGACTCTACATTGTATAAGAACTTATTGTG	1860
a	N I F K N C L K E I D S T L Y K N L F V	-
1861	GATAAGAAATATGAAGTATATTCACACAGAAGATGTTTCAGGCTGTCTGCTGGAAGACAA	1920
a	D K N M K Y I P T E D V S G L S L E E Q	-
1921	TTGAGGAGGTGCAAGAAACGAACCTTGTAAGTGTTGATGGACAAAGATTCTGTT	1980
a	L R R L Q E E R T C K V C M D K E V S V	-
1981	GTATTATTCCCTTGTGTCATCTGGTAGTATGCCAGGAATGTGCCCTTCTCTAAGAAA	2040
a	V F I P C G H L V V C Q E C A P S L R K	-
2041	TGCCCTATTTCAGGGGTATAATCAAGGGTACTGTTCTGTACATTCTCTTAAAGAAA	2100
a	C P I C R G I I K G T V R T F L S *	-
2101	ATAGTCTATATTTAACCTGCATAAAAGGCTTTAAATAATTGTGAACACTTGAAGCC	2160
a		-

Fig. 3 (page 6 of 7)

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HUMAN hiap-2

2161	ATCTAAAGTAAAGGGAATTATGAGTTTTCATTAAGTAACATTCATGTTCTAGTCTGC	2220
a	-	-
2221	TTTGGTACTAATAATCTTGTCTGAAAGATGGTATCATATATTTAATCTTAATCTGTT	2280
a	-	-
2281	TATTACAAGGGAAGATTATGTTTGGTGAACATAATAGTATGTGTACCTAAGGG	2340
a	-	-
2341	AGTAGCGTCXCTGCTTGTATGCATCATTTCCAGGAGTACTGGATTGTGTTCTTTCAG	2400
a	-	-
2401	AAAGCTTTGAAXACTAAATTATAGTGTAGAAAGAACTGGAAACCAGGAACCTCTGGAGTT	2460
a	-	-
2461	CATCAGAGTTATGGTGCCGAATTGTCTTTGGTGCTTTTCACCTTGTTTAAATAAGGA	2520
a	-	-
2521	TTTTTCTCTTATTTCTCCCCCTAGTTTGTGAGAAACATCTCAATAAAGTGCTTTAAAG	2580
a	-	-

Fig. 3 (page 7 of 7)

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MOUSE xiap

```
361      GCTGTTGGAAGACACAGGAGAAATATCCCAAAATTCAGATTATCAATGGTTTATTTT 420
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      A V G R H R R I S P N C R F I N G F Y F -

421      GAAAATGGTGCTGCACAGTCTACAAATCCTGGTATCCAAATGGCCAGTACAAATCTGAA 480
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      E N G A A Q S T N P G I Q N G Q Y K S E -

481      AACTGTGTGGAAATAGAAATCCTTTTGCCCTGACAGGCCACCTGAGACTCATGCTGAT 540
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      N C V G N R N P F A P D R P P E T H A D -

541      TATCTCTGAGAACTGGACAGGTTGTAGATATTTCAGACACCATATACCCGAGGAACCT 600
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      Y L L R T G Q V V D I S D T I Y P R N P -

601      GCCATGTGTAGTGAAGAACCCAGATTGAAGTCATTTTCAGAACTGGCCGGACTATGCTCAT 660
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      A M C S E E A R L K S F Q N W P D Y A H -

661      TTAACCCAGAGAGTTAGCTAGTGTGGCCTCTACTACAGGGGCTGATGATCAAGTG 720
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
a      L T P R E L A S A G L Y Y T G A D D Q V -
```

Fig. 4 (page 2 of 6)

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MOUSE xiap

```
721 CAATGCTTTTGTGGGAAACTGAAATAATTGGGAACCTGTGATCGTGCCCTGGTCA 780
-----+-----+-----+-----+-----+-----+-----+
a Q C F C C G G K L K N W E P C D R A W S -

781 GAACACAGGAGACACTTCCCAATTGCTTTTGTGTTTGGGCCGGAACGTTAATGTTCTGA 840
-----+-----+-----+-----+-----+-----+-----+
a E H R R H F P N C F F V L G R N V N V R -

841 AGTGAATCTGGTGTGAGTTCTGATAGGAATTCCCAAAATTCAACTCTCCAAGAAAT 900
-----+-----+-----+-----+-----+-----+-----+
a S E S G V S S D R N F P N S T N S P R N -

901 CCAGCCATGGCAGAAATATGAAGCACGGATCGTTACTTTTGGAAATGATATACAGTT 960
-----+-----+-----+-----+-----+-----+-----+
a P A M A E Y E A R I V T F G T W I Y S V -

961 AACAGGAGCAGCTTGCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAG 1020
-----+-----+-----+-----+-----+-----+-----+
a N K E Q L A R A G F Y A L G E G D K V K -

1021 TGCTTCCACTGTGGAGGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGGACCAG 1080
-----+-----+-----+-----+-----+-----+-----+
a C F H C G G G L T D W K P S E D P W D Q -
```

Fig. 4 (page 3 of 6)

MOUSE xiap

1081	CATGCTAAGTGCTACCCAGGTGCAAAATACCTATTGGATGAGAAGGGCAAGAAATATATA	1140
a	H A K C Y P G C K Y L L D E K G Q E Y I	-
1141	AAATAATTCATTAAACCCTCCACTTGAGGAATCTTTGGGAAGAACTGCTGAAAAACA	1200
a	N N I H L T H P L E E S L G R T A E K T	-
1201	CCACCGCTAACTAAAAAATCGATGATACCATCTTCCAGAAATCCTATGGTGCAAGAAGCT	1260
a	P P L T K K I D D T I F Q N P M V Q E A	-
1261	ATACGAATGGGATTAGCTTCAAGGACCTTAAGAAAAACAATGGAAGAAAAATCCAAACA	1320
a	I R M G F S F K D L K K T M E E K I Q T	-
1321	TCCGGGAGCAGCTATCTACTTGAAGTCCCTGATTGCAGATCTTGTGAGTGCTCAGAAA	1380
a	S G S S Y L S L E V L I A D L V S A Q K	-
1381	GATAATACGGAGGATGAGTCAAGTCAAACCTTCATTGCAGAAAGACATTAGTACTGAAGAG	1440
a	D N T E D E S S Q T S L Q K D I S T E E	-

Fig. 4 (page 4 of 6)

MOUSE xiap

1441	CAGCTAAGCGCCTACAAGAGAGAGCTTTC	A A A T C T G T A T G G A T A G A A T A T T G C T	1500
a	Q L R R L Q E E K L S K I C M D R N I A	-	
1501	ATCGTTTTTTCCTTGCGACATCTGGCCACTTG	T A A C A G T G T G C A G A A G C A G T T G A C	1560
a	I V F F P C G H L A T C K Q C A E A V D	-	
1561	AAATGTCCCATGTGCTACACCGTCATTACGTT	C A C C A A A A A T T T T A T G T C T T A G T G G	1620
a	K C P M C Y T V I T F N Q K I F M S *	-	
1621	GGCACCATGTTATGTTCTTCTTGCTCTAATTG	A A T G G A T G G A G C C A A C T T T A A G	1680
a		-	
1681	TAACTCCGCAATTGCATTCCATTAGCATCCTG	C T G T T T C C A A A T G G A G A C C A A T G C T A A C	1740
a		-	
1741	AGCACTGTTCCGCTAAACATTCAATTCTGGAT	C T T T C G A G T T A T C A G C T G T A T C A T T	1800
a		-	

Fig. 4 (page 5 of 6)

1801	TAGCCAGTGTTTTACTCGATTGAAACCTTAGACAGAGAAGCATTTTATAGCTTTTCACAT	1860
a	-	-
1861	GTATATTGGTAGTACACTGACTTGATTCTATATGTAAGTGAATTCATCACCTGCATGTT	1920
a	-	-
1921	TCATGCCCTTTTGCATAAGCTTAACAAATGGAGTGTCTGTATAAGCATGGAGATGTGATG	1980
a	-	-
1981	GAACTGCCCAATGACTTTAAATTGGCTTATTGTAAACACGGAAGAAGTCCCCACGCTG	2040
a	-	-
2041	CTGGGAGGATAAAGATTGTTTTAGATGCTCACTTCTGTGTTTTAGGATCTGCCCATTTA	2100

Fig. 4 (page 6 of 6)

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M-hiap-1

```
SEQ ID NO:39      GAATTCGGGAGACCTACACCCCGGAGATCAGAGGTCA TTGCTGGCGTTCAGAGCCTAG
1  -----+-----+-----+-----+-----+-----+-----+ 60
   GAAGTGGGCTGCCGTATCAGCCTAGCAGTAAACCGACCAGAGCCATGCACAAACTAC
61 -----+-----+-----+-----+-----+-----+-----+ 120
   ATCCCAGAGAAAGACTTGTCCTTCCCTCCCTGTCACTCACCATGAACATGGTTCAA
121 -----+-----+-----+-----+-----+-----+-----+ 180
                               M N M V Q -

SEQ ID NO:40      GACAGCGCCTTTCTAGCCAAGCTGATGAAGAGTGCTGACACCTTTGAGTTGAAGTATGAC
181 +-----+-----+-----+-----+-----+-----+-----+ 240
   D S A F L A K L M K S A D T F E L K Y D -
                               TTTTCCTGTGAGCTGTACCGATTGTCCACGTA TTCAGCTTTTCCAGGGAGTTCCTGTG
241 +-----+-----+-----+-----+-----+-----+-----+ 300
   F S C E L Y R L S T Y S A F D R G V P V -
                               TCAGAAAGGAGCTGGCTCGTGGCTTTTACTACACTGGTGCCAATGACAAGGTCAAG
301 +-----+-----+-----+-----+-----+-----+-----+ 360
   S E R S L A R A G F Y Y T G A N D K V K -
                               TGCTTCTGCTGGCCTGATGCTAGACAAC TGGAAACAAGGGACAGTCCCATGGAGAAG
361 +-----+-----+-----+-----+-----+-----+-----+ 420
   C F C C G L M L D N W K Q G D S P M E K -
```

Fig. 5 (page 1 of 6)

M-hiap-1

```

421 CACAGAAAGTTGTACCCAGCTGCAACTTGTACAGACTTGAATCCAGCCAACAGTCTG
      H R K L Y P S C N F V Q T L N P A N S L - 480
481 GAAGCTAGTCCTCGGCCTTCTCTCTCCACGGCGATGAGCACCATGCCCTTGAGCTTT
      E A S P R P S L P S T A M S T M P L S F - 540
541 GCAAGTCTGAGAATACTGGCTATTTCAGTGGCTCTTACTCGAGCTTCCCTCAGACCCT
      A S S E N T G Y F S G S Y S S F P S D P - 600
601 GTGAACTCCGAGCAAAATCAAGATTGTCCTTGCTTTGAGCACAAGTCCCTACCACCTTGCA
      V N F R A N Q D C P A L S T S P Y H F A - 660
661 ATGAACACAGAGAAGCCAGATTACTCACCTATGAACAATGGCCATTGCTTTCTGTCA
      M N T E K A R L L T Y E T W P L S F L S - 720
721 CCAGCAAAGCTGGCCAAAGCAGGCTTCTACTACATAGGACCTGGAGATAGAGTGGCCTGC
      P A K L A K A G F Y Y I G P G D R V A C - 780
```

Fig. 5 (page 2 of 6)

M-hiap-1

```
781 TTTGCGTGGGAACTGAGCAACTGGGAACGTAAGGATGATGCTATGTCAGAGCAC 840
    F A C D G K L S N W E R K D D A M S E H -
841 CAGAGGCATTCCCCAGCTGTCCGTTCTTALLkGACTTGGGTCAGTCTGCTTCGAGATAC 900
    Q R H F P S C P F L K D L G Q S A S R Y -
901 ACTGTCTCTAACCTGAGCATGCAGACACGCGAGCCCGTATTAGAACATTCTCTAACTGG 960
    T V S N L S M Q T H A A R I R T F S N W -
961 CCTTCTAGTGCACTAGTTCAATCCAGGAAGTGGGCTTTTATTATACAGGA 1020
    P S S A L V H S Q E L A S A G F Y Y T G -
1021 CACAGTGATGTCAAGTGTTTATGCTGTGATGGTGGGCTGAGGTGCTGGGAATCTGGA 1080
    H S D D V K C L C C D G G L R C W E S G -
1081 GATGACCCCTGGGTGGAACATGCCAAGTGGTTTCCAAGGTGTGAGTACTTGCTCAGAATC 1140
    D D P W V E H A K W F P R C E Y L L R I -
1141 AAAGGCCAAGAATTGTCAGCCAAGTTCAGCTGGCTATCCTCATCTACTTGAGCAGCTA 1200
    K G Q E F V S Q V Q A G Y P H L L E Q L -
```

Fig. 5 (page 3 of 6)

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M-hiap-1

```
1201 TTATCTACGTCAGACTCCCAGAAGATGAGAATGCAGACGCAATCGTGCAATTTGGC + 1260
    L S T S D S P E D E N A D A A I V H F G -
1261 CCTGGAGAAAGTTCGGAAGATGTCGTCAATGATGAGCAGCCTGTGGTTAAAGCAGCCTTG +
    P G E S S E D V V M M S T P V V K A A L -
1321 GAAATGGGCTTCAGTAGAGCCTGGTGAGACAGACGGTTCAGTGGCAGATCCTGGCCACT + 1380
    E M G E S R S L V R Q T V Q W Q I L A T -
1381 GGTGAGAACTACAGGACCGTCAGTGACCTCGTTATAGGCTTACTCGATGCAGAAGACGAG + 1440
    G E N Y R T V S D L V I G L L D A E D E -
1441 ATGAGAGAGGAGCAGATGGAGCAGCGCGCCGAGGAGGAGTCAATGATCTAGCACTA + 1500
    M R E E Q M E Q A A E E E S D D L A L -
1501 ATCCGGAAGAAATAATGGTGCTTTTCCAAACATTTGACGTGTGTGACACCAATGCTGTAT + 1560
    I R K N K M V L F Q H L T C V T P M L Y -
```

Fig. 5 (page 4 of 6)

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M-hiap-1

```
1561  TGCCTCCTAAGTCAAGGCCATCACTGAACAGGAGTGCAATGCTGTGAACAGAAACCA 1620
      C L L S A R A I T E Q E C N A V K Q K P -
1621  CACACCTTACAAGCAAGCACACTGATTGATACTGTGTTAGCAAAAGGAAACACTGCAGCA 1680
      H T L Q A S T L I D T V L A K G N T A A -
1681  ACCTCATTCAGAAACTCCCTTCGGAAATTGACCCCTGCGTTATACAGAGATATATTGTG 1740
      T S F R N S L R E I D P A L Y R D I F V -
1741  CAACAGGACATTAGAGTCTTCCACAGATGACATTGCAGCTCTACCAATGGAAGAACAG 1800
      Q Q D I R S L P T D D I A A L P M E E Q -
1801  TTGCGGCCCTCCCGAGGACAGAATGTGTAAGTGTGTATGGACCGAGAGGTATCCATC 1860
      L R P L P E D R M C K V C M D R E V S I -
1861  GTGTTTCATTCCTGTGGCCATCTGGTCGTGTGCAAAAGACTCGGCTCCCTCTCTGAGGAAG 1920
      V F I P C G H L V V C K D C A P S L R K -
```

Fig. 5 (page 5 of 6)

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M-hiap-1

```
1921 TGTCCCATCTGTAGAGGACCATCAAGGCACAGTGGCACATTTCTCTCCTGAACAAGA 1980
-----+-----+-----+-----+-----+-----+-----+
C P I C R G T I K G T V R T F L S *
1981 CTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCACCTGTCACCTCCAGTTCCAT 2040
-----+-----+-----+-----+-----+-----+-----+
TCGGAACCTTGAGGCCAGCCTGGATAGCACGAGACACCGCCAAACKCACAAATATAAACAT
2041 -----+-----+-----+-----+-----+-----+-----+ 2100
GAAAAA CTTTGTCTGAAGTCAAGAATGAATGAATTAATAATAATTTAATTGGT
2101 -----+-----+-----+-----+-----+-----+-----+ 2160
TTCCTTAAAGTGCTATTGTTCCCAACTCAGAAAATTGTTTCTGTAAACATATTTACA
2161 -----+-----+-----+-----+-----+-----+-----+ 2220
TACTACCTGCATCTAAAGTATTCTATATATTCATATATTCAGATGTCATGAGAGGGTTT
2221 -----+-----+-----+-----+-----+-----+-----+ 2280
TGTTCTTGTTCTGAAAAGCTGGTTTATCATCTGATCAGCATATACTGCCAACGGGCAG
2281 -----+-----+-----+-----+-----+-----+-----+ 2340
GGCTAGAAATCCATGAACCAAGCTGCAAGATCTCACGCTAAATAAGCGGAAAGATTGG
2341 -----+-----+-----+-----+-----+-----+-----+ 2400
AGAAACGAAAGGAAATTCTTTCCTGTCCAATGTATACTCTTCAGACTAATGACCTCTTCC
2401 -----+-----+-----+-----+-----+-----+-----+ 2460
TATCAAGCCTTCTA
2461 -----+-----+-----+-----+-----+-----+-----+ 2474
```

Fig. 5 (page 6 of 6)

M-hiap-2

Fig. 6 (page 1 of 6)

M-hiap-2

```

421 GACTCTGCTTTCAGCCAGTCTGCAGTCTCCATCTAAGAAATATGTCTCTCTGTGAAAGTAG
      T L L S A S L Q S P S K N M S P V K S R - 480
481 ATTTGCACATTGTCACCTCTGGAACGAGGTGGCATTCACTCCAACCTGTGCTCTAGCCC
      F A H S S P L E R G G I H S N L C S S P - 540
541 TCTTAATTCTAGACAGTGAAGACTTCTCATCAAGGATGGATCCCTGCAGCTATGCCAT
      L N S R A V E D F S S R M D P C S Y A M - 600
601 GAGTACAGAAGGCCAGATTCTTACTTACAGTATGTGGCCTTTAAGTTTCTGTCACC
      S T E E A R F L T Y S M W P L S F L S P - 660
661 AGCAGAGCTGGCCAGAGCTGGCTTCTATTACATAGGCCCTGGAGACAGGGTGGCCTGTTT
      A E L A R A G F Y Y I G P G D R V A C F - 720
721 TGCCTGTGTGGAAACTGAGCAACTGGGAACCAAGGATTATGCTATGTCAGAGCACCG
      A C G G K L S N W E P K D Y A M S E H R - 780
```

Fig. 6 (page 2 of 6)

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M-hiap-2

```
781 CAGACATTTCCCACTGTCCATTCTGGAAATACTTCAGAAACACAGAGGTTAGTAT + 840
    R H F P H C P F L E N T S E T Q R F S I -
841 ATCAAATCTAAGTATGCAGACACACTCTGCTCGATTGAGGACATTTCTGTACTGGCCACC + 900
    S N L S M Q T H S A R L R T F L Y W P P -
901 TAGTGTTCCTGTTCAGCCCGAGCAGCTTGCAAGTCTGGATTCTATTACGTGGATCGCRA + 960
    S V P V Q P E Q L A S A G F Y Y V D R N -
961 TGATGATGTCAAGTGCCTTTGTTGTGATGGTGGCTTGAGATGTTGGGAACCTGGAGATGA + 1020
    D D V K C L C C D G G L R C W E P G D D -
1021 CCCCTGGATAGAACACGCCAAATGGTTTCCAAGGTGTGAGTTCTTGATACGGATGAAGGG + 1080
    P W I E H A K W F P R C E F L I R M K G -
1081 TCAGGAGTTTGTGATGAGATTCAAGCTAGATATCCTCATCTTCTTGAGCAGCTGTTGTC + 1140
    Q E F V D E I Q A R Y P H L L E Q L L S -
```

Fig. 6 (page 3 of 6)

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M-hiap-2

```
1141 CACTTCAGACACCCAGGAGAGAAATGCTGACCTACAGACAGTGGTGCATTG 1200
      -----+-----+-----+-----+-----+-----+
      T S D T P G E E N A D P T E T V V H F G -

1201 CCCTGGAGAAAGTTCGAAAGATGTCGTCATGATGAGCAGCCTGTGTTAAAGCAGCCTT 1260
      -----+-----+-----+-----+-----+-----+
      P G E S S K D V V M M S T P V V K A A L -

1261 GGAAATGGGCTTCAGTAGGAGCCTGGTGAGACAGCGGTTCAGCGGCAGATCCTGGCCAC 1320
      -----+-----+-----+-----+-----+-----+
      E M G F S R S L V R Q T V Q R Q I L A T -

1321 TGGTGAGAACTACAGGACCGTCAATGATATTGTCTCAGTACTTTTGAATGCTGAAGATGA 1380
      -----+-----+-----+-----+-----+-----+
      G E N Y R T V N D I V S V L L N A E D E -

1381 GAGAAGAGAAGAGGAGAAAGACAGACTGAAGAGATGGCATCAGGTGACTTATCACT 1440
      -----+-----+-----+-----+-----+-----+
      R R E E E K E R Q T E E M A S G D L S L -

1441 GATTCGGAAGAATAGAAATGGCCCTCTTTCAACAGTTGACACATGTCCTTCCTATCCTGGA 1500
      -----+-----+-----+-----+-----+-----+
      I R K N R M A L E Q Q L T H V L P I L D -
```

Fig. 6 (page 4 of 6)

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M-hiap-2

```
1501 TAATCTTCTTGAGCCAGTGTAATTACAAACAGGAACATGATATTATTAGACAGAAAC
-----+-----+-----+-----+-----+-----+ 1560
      N L L E A S V I T K Q E H D I I R Q K T -

1561 ACAGATACCCTTACAAGCAAGAGAGCCTTATTGACACCGTTTAGTCAAGGGAATGCTGC
-----+-----+-----+-----+-----+-----+ 1620
      Q I P L Q A R E L I D T V L V K G N A A -

1621 AGCCAACATCTTCAAAAACCTCTGAAGGGAATTGACTCCACGTTATATGAAACTTATT
-----+-----+-----+-----+-----+-----+ 1680
      A N I F K N S L K G I D S T L Y E N L F -

1681 TGTGAAAAGAATATGAAGTATATCCAACAGAAGACGTTTCAGGCTTGTCATTGGAAGA
-----+-----+-----+-----+-----+-----+ 1740
      V E K N M K Y I P T E D V S G L S L E E -

1741 GCAGTTGCGGAGATTACAAGAAGAACGAACTTGCAAGTGTTGACAGAGAGGTTTC
-----+-----+-----+-----+-----+-----+ 1800
      Q L R R L Q E E R T C K V C M D R E V S -

1801 TATTGTGTTCAATCCGTGTGGTCATCTAGTAGTCTGCCAGGAATGTGCCCTTCTCTAAG
-----+-----+-----+-----+-----+-----+ 1860
      I V F I P C G H L V V C Q E C A P S L R -
```

Fig. 6 (page 5 of 6)

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M-hiap-2

```
1861 GAAGTGCCCATCTCAGGGGACAATCAAGGGACTGTGCGCACATTCTCTCATGAGT 1920
      K C P I C R G T I K G T V R T F L S * -
1921 GAAGAAATGGTCTGAAAGTATTGTTGGACATCAGAAGCTGTCAGAACAAAGAATGAAC TAC 1980
      TGATTTCAGCTCTTCAGCAGGACATTCTACTCTCTTCAAGATTAGTAATCTTGCTTTAT
1981 GAAGGGTAGCATTGTATATTAAAGCTTAGTCTGTTGCAAGGGAAGGCTCTATGCTGTTGAG 2040
      CTACAGGACTGTGTCTGTTCCAGAGCAGGAGTTGGGATGCTTGCTGTATGTCCTTCAGGA 2100
2101 CTTCTTGGGATTTGGGAATTTGGGGAAAGCTTTGGAAATCCAGTGATGTGGAGCTCAGAAA 2160
      TCCTGGAACCACTCTGGTACTCAGTAGATAGGGTACCCTGTACTTCTTGCTGCTTT 2220
2221 TCCAGTCTGGGAAATAAGGAGGAATCTGCTGCTGTAATAAATTGCTGGATGTGAGAAAT 2280
      AGATGAAAGTGTTCGGGTGGGGCCGTGCATCAGTGTAGTGTGCAGGGATGTATGCAG 2340
2341 GCCAAACACTGTGTAG
2401 -----+----- 2416
```

Fig. 6 (page 6 of 6)

Alignment of BIR (Baculoviral IAP Repeats) Domains

Baculovirus
Cp_iap
Op_iap
Human
xiap
hiap1, hiap2
Mouse
m-xiap
Insect
diap

Cydia pomonella
Orgyia pseudotsugata
IAP on X chromosome
two different human IAP genes
mouse homologue of human xiap gene
Drosophila IAP gene, not clearly a homologue of xiap or hiap

Fig. 7

note on consensus: The consensus line represents amino acids or very similar amino acids which are present in 14 of the 19 BIR sequences at each position.
Capitalized residues are those that are in the consensus sequence.

SEQ ID NO:11	Op_iap-1	1	kaaRLgTYtn	WPvqf.l	leps	rMAasGFYYL	GrgDeVrCaf	CkveitnWvr	gDdpetdHkr	waPqCpFV	41/61
SEQ ID NO:14	Cp_iap-1		eevRLnTFek	WPvsf.l	lspe	tMAknGFYYL	GrsDeVrCaf	CkveimrWke	gEdpaadHkk	waPqCpFV	
SEQ ID NO:15	diap-2		eanRLvTFkd	WPnnpn.i	Lpq	aLakAGFFYYL	nrlDhVkcVw	CngviakWek	nDnafeeHkr	ffPqCpRV	
SEQ ID NO:16	m-xiap-1		efnRLkTFan	FPssspvsas		tLARAGFLYt	GegDtVqCFs	ChaaidrWqy	gDsavgrHrr	isPnCrFI	
SEQ ID NO:17	xiap-1		efnRLkTFan	FPsgspvsas		tLARAGFLYt	GegDtVrCFs	ChaaivrWqy	gDsavgrHrk	vsPnCrFI	
SEQ ID NO:18	hiap1-1		elyRMstYst	FPagvpvser		sLARAGFFYt	GvnDkVkcFCf	CglmldnWkr	gDsptekHkk	lyPsCrFV	
SEQ ID NO:19	hiap2-1		elyRMstYst	FPagvpvser		sLARAGFFYt	GvnDkVkcFCf	CglmldnWkl	gDspiqkHkq	lyPsCsFI	
SEQ ID NO:20	m-xiap-2		eearLksFqn	WPdyahltptr		eLASAGLLYt	GadDqVqCFc	CggklknWep	cDrawseHrr	hfpnCffv	
SEQ ID NO:21	xiap-2		eearLksFqn	WPdyahltptr		eLASAGLLYt	GigDqVqCFc	CggklknWep	cDrawseHrr	hfpnCffv	
SEQ ID NO:22	hiap1-2		enaRLlTFqt	WP.lLflspt		dLARAGFFYi	GpgDrVaCfa	CggklknWep	kDnamseHlr	hfpkCpFI	
SEQ ID NO:23	hiap2-2		eearFlTYhm	WP.lLflsps		eLARAGFFYi	GpgDrVaCfa	CggklknWep	kDdamseHrr	hfpnCpFl	
SEQ ID NO:24	m-xiap-3		yeaRivTFgt	Wiyv..nke		qLARAGFYal	GegDkVkcCFh	CgggltdWkp	sEdpwdqHak	cYPgCkYl	
SEQ ID NO:25	xiap-3		yeaRifTFgt	Wiyv..nke		qLARAGFYal	GegDkVkcCFh	CgggltdWkp	sEdpweqHak	wYPgCkYl	
SEQ ID NO:26	hiap1-3		haaRFkTFfn	WPssvlvnpe		qLASAGFFYv	GnsDdVkcCFc	CdggllrcWes	gDdpwvqHak	wfPrCeYl	
SEQ ID NO:27	hiap2-3		haaRMrTFmy	WPssvpvqpe		qLASAGFFYv	GrnDdVkcCFg	CdggllrcWes	gDdpwveHak	wfPrCeFl	
SEQ ID NO:28	Op_iap-2		eaarLrTFae	WPrglkqrpe		eLAeAGFFYt	GqgDktrCFc	CdggllkdWep	dDapwqqHar	wydrCeYV	
SEQ ID NO:29	Cp_iap-2		eaarVksFhn	WPrcmkqrpe		qMAdAGFFYt	GygDntkCFy	CdggllkdWep	eDvpweqHvr	widrCaYV	
SEQ ID NO:30	diap-3		vdaRLrTFtd	WPisniqpas		aLAqAGLYYq	kigDqVrCFh	Cniglrswqk	eDepwieHak	wsPkCqFV	
SEQ ID NO:31	diap-1		esvRLaTFge	WPlnapvsae		dLvanGFF..	GtwmeaeCdf	ChvrldrWey	gDlvaerHrr	ssPiCsmV	
SEQ ID NO:2	Consensus		---RL-TF--	WP-----	-----	-LA-AGFFY-	G--D-V-CF-	C-----W--	-D-----H--	--P-C-FV	

Fig. 8 (page 1 of 5)

Fig. 8 (page 2 of 5)

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BIR 3		301	350
cp-iap	qrpeQMAAdAG	FFYtGyGDnt	KCFyCdGGLk dWepeDvPWe QHvrWFdrCa
diap	qpasaLAqAG	LYYqkiGdqv	rCFhCniGLr sWqkeDEPwf eHAKWSPkCq
m-xiap	VnkeQLARAG	FYalGeGDkV	KCFhCgGGLt dwkpsEDPwD QHAKcYPgCk
xiap	VnkeQLARAG	FYalGeGDkV	KCFhCgGGLt dwkpsEDPwD QHAKWYPgCk
hiap1	VnpEQLASAG	FYYvGnsDdV	KCFcCdGGLr cWesgDDPwV QHAKWFPrCe
hiap2	VqpEQLASAG	FYYvGRsDdV	KCFgCdGGLr cWesgDDPwV eHAKWFPrCe
consensus	V--EQLA-AG	FYY-G-GD-V	KCF-C-GGL- -W---DDPW- QHAKWFP-C-
		351	400
cp-iap	YVqlvKGrDY	VqkVit.....e.....
diap	FvllakGpay	VseVlattaA	nassqpaTap aptlq.....
m-xiap	YLldeKGQeY	InnIhlthp.	LeEsLgrTae kt.....Ppltk
xiap	YLleqKGQeY	InnIhlths.	LeEcLvrTte kt.....Psltr
hiap1	YLlriKGQeY	IrqVqasyph	LlEqLlstsD spgdenaess iihlePgedh
hiap2	FLlrmKGQeF	VdeIqgryph	LlEqLlstsD ttgeenadpp iihfgPgess
consensus	YL---KGQeY	-----L-E-L--T--	-----P-----
		401	450
cp-iap	..acVLpge.
diap	..adVLmdea	pakeAltLGi	dggvVrnaiaq rKllssGcaF stldeLlhDi
m-xiap	kiDdtifqnP	mVqeAirMGF	sfkdIKktme eKIqtsGssY lslevLIaDL
xiap	riDdtifqnP	mVqeAirMGF	sfkdIKkime eKIqisGsnY kslevLVaDL
hiap1	seDaIMmntP	vInaAveMGF	srsLVKqtvq rKIlatGenY rlvndLVlDL
hiap2	seDaVMmntP	vVksAleMGF	nrdLVKqtvI sKIlttGenY ktvndiVsaL
consensus	--D-V----P	-V--A--MGF	-----VK----- -KI---G--Y -----LV-DL

Fig. 8 (page 3 of 5)

Fig. 8 (sheet 4 of 5)

		Ring Zinc Finger	
cp-iap diap m-xiap xiap hiap1 hiap2 consensus	551	600
	..:tki..:..	..:..	Ekep
	sniskitdei	nlslEEnRq	veDskLCKIC yveEciVcFV
	diStEEQLRR	LkDarLCKVC LDeEVgVVF1
	eiStEEQLRR	LqEEkLsKIC MDrnIaIVFf
	lyehlfvqgd	dlpvEEQLRR	LqEEkLCKIC MDrnIaIVFV
	lyknlfvdkn	glSlEEQLRR	LpEErtCKVC MDkEVsIVFI
cp-iap diap m-xiap xiap hiap1 hiap2 consensus	601	---S-EEQLRR	MDkEVsVVF1
	PCGHLV-V-C--	---	MD-EV--VF-
	PCGHLV-V-C--	---	MD-EV--VF-
	PCGHLV-V-C--	---	MD-EV--VF-
	PCGHLV-V-C--	---	MD-EV--VF-
	PCGHLV-V-C--	---	MD-EV--VF-
	PCGHLV-V-C--	---	MD-EV--VF-
cp-iap diap m-xiap xiap hiap1 hiap2 consensus	635	CRkIVtSVlk	veDskLCKIC yveEciVcFV
	PCGHLV-V-C--	CRkIVtSVlk	LkDarLCKVC LDeEVgVVF1
	PCGHLV-V-C--	CRkIVtSVlk	LqEEkLsKIC MDrnIaIVFf
	PCGHLV-V-C--	CRkIVtSVlk	LqEEkLCKIC MDrnIaIVFV
	PCGHLV-V-C--	CRkIVtSVlk	LpEErtCKVC MDkEVsIVFI
	PCGHLV-V-C--	CRkIVtSVlk	MDkEVsVVF1
	PCGHLV-V-C--	CRkIVtSVlk	MD-EV--VF-

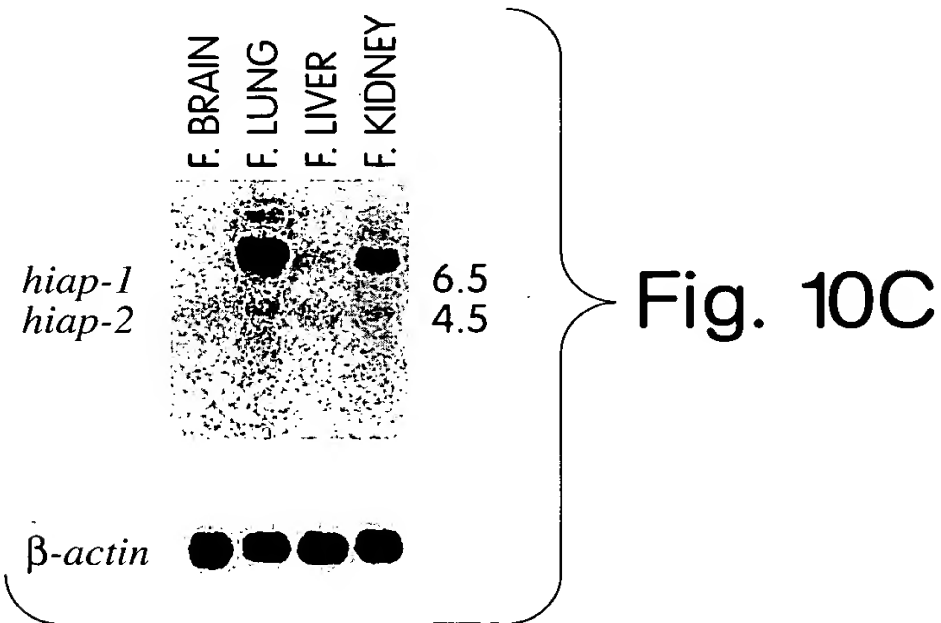
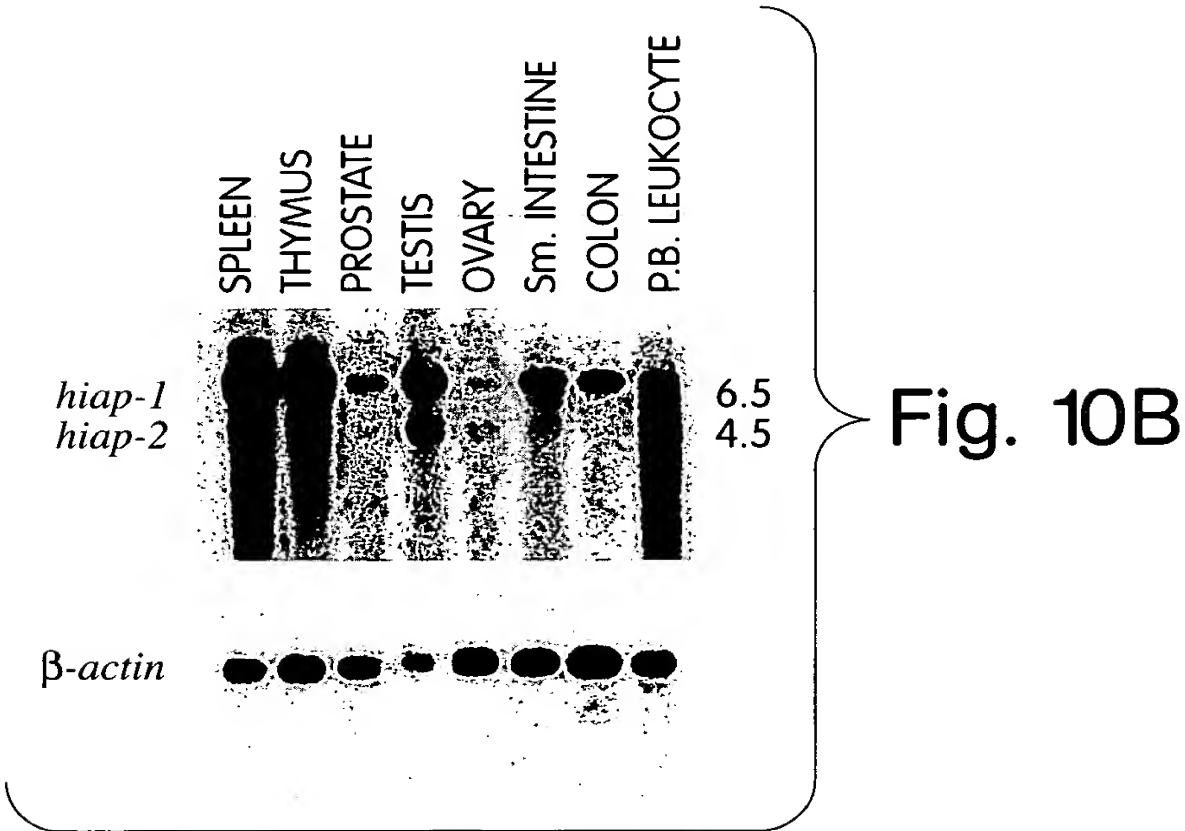
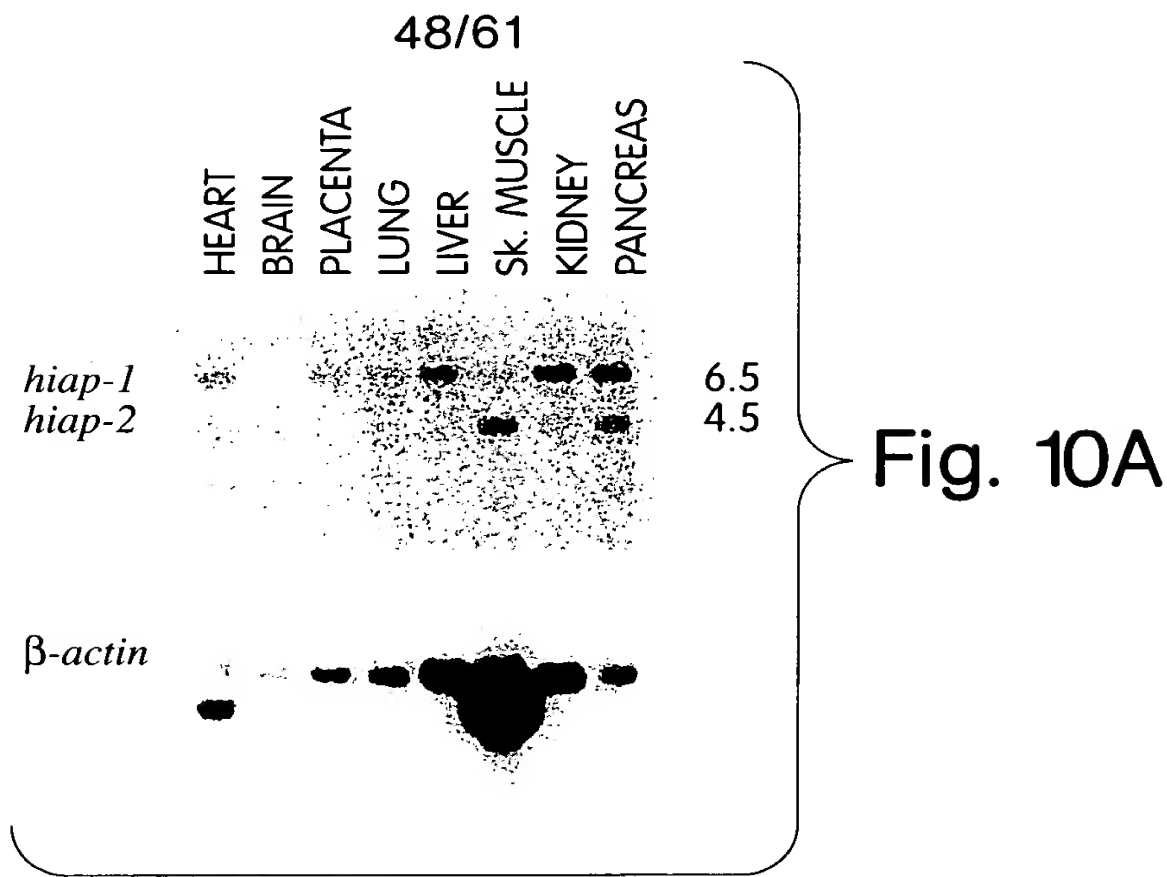
Fig. 8 (sheet 5 of 5)

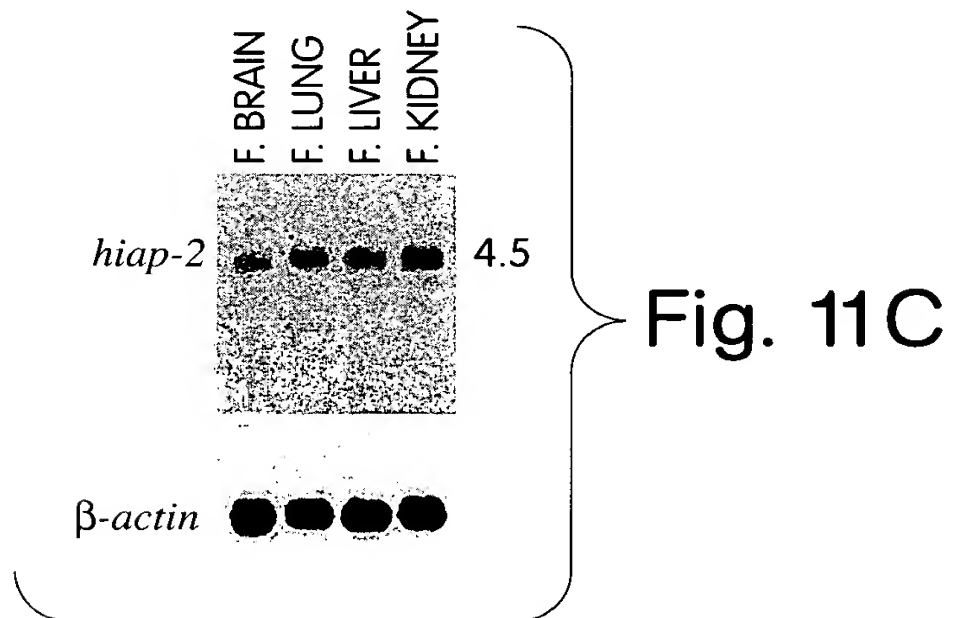
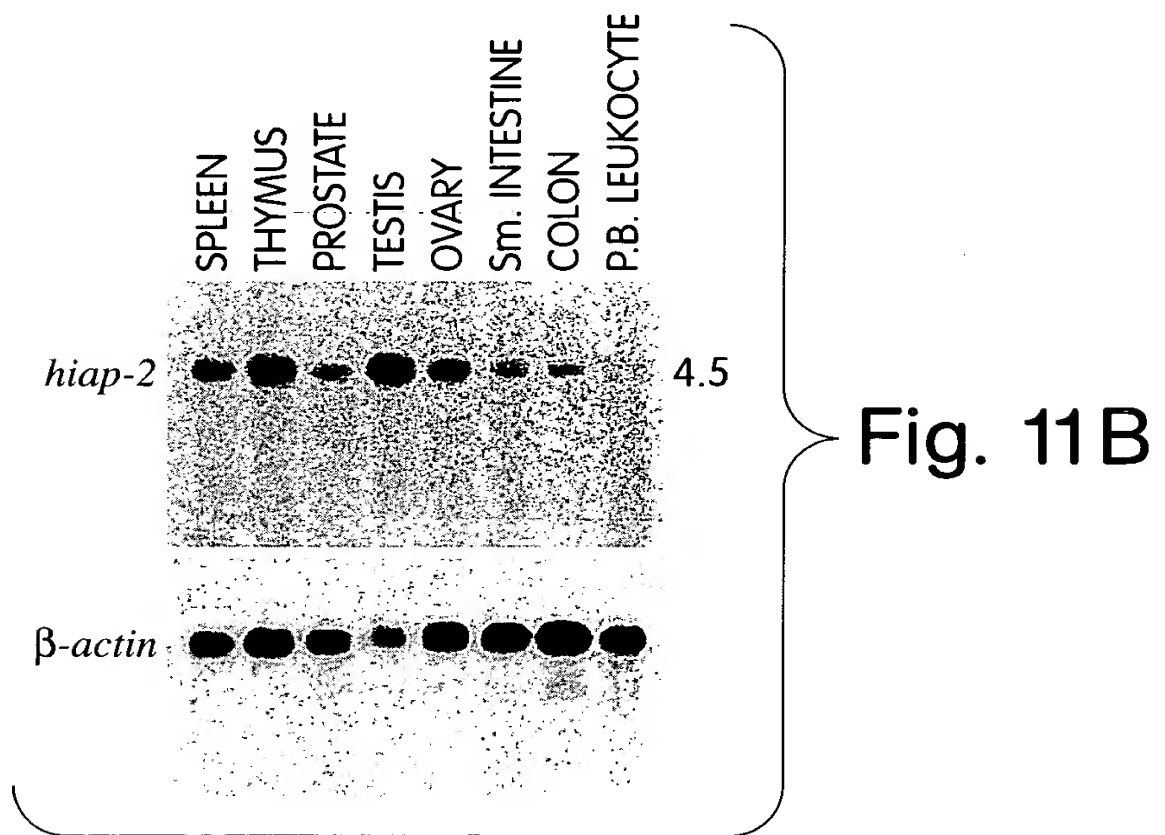
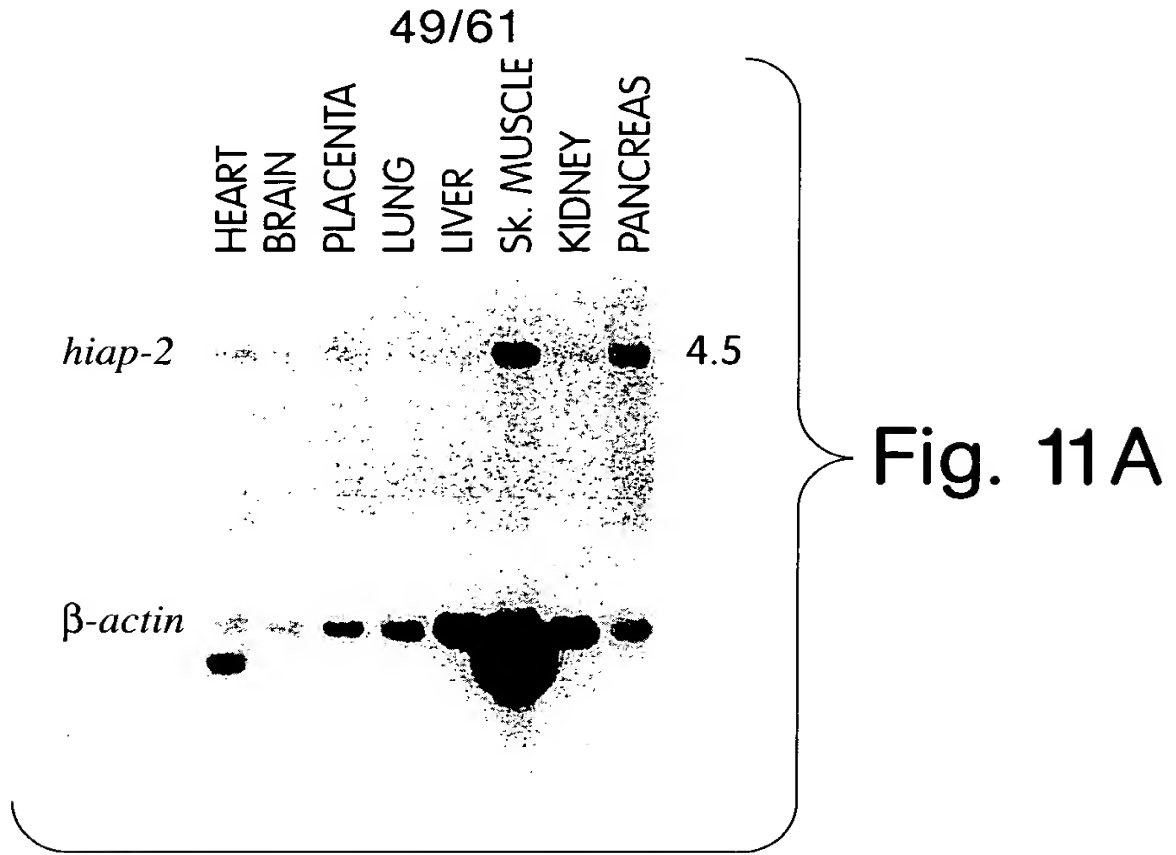
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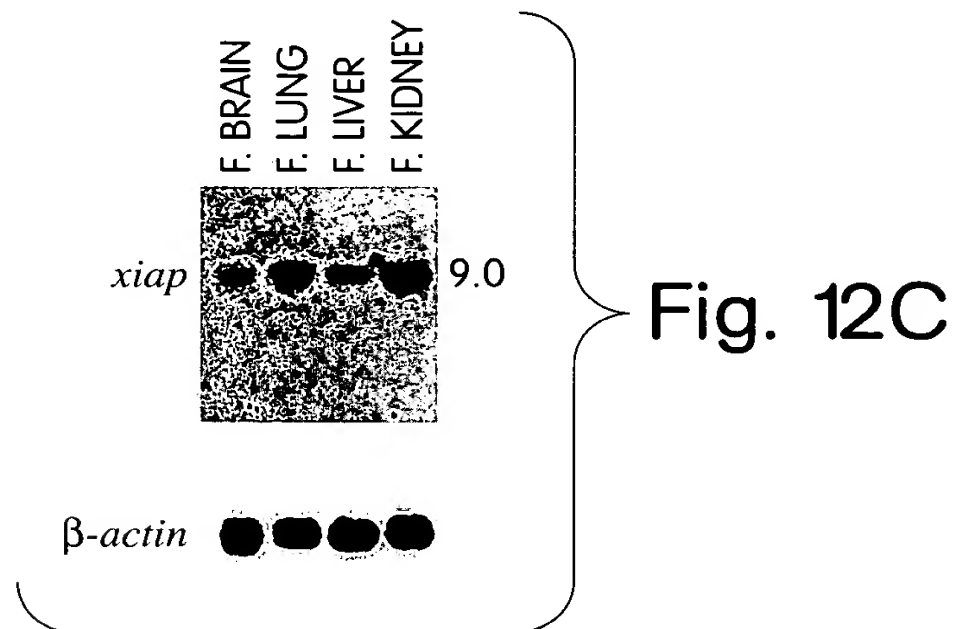
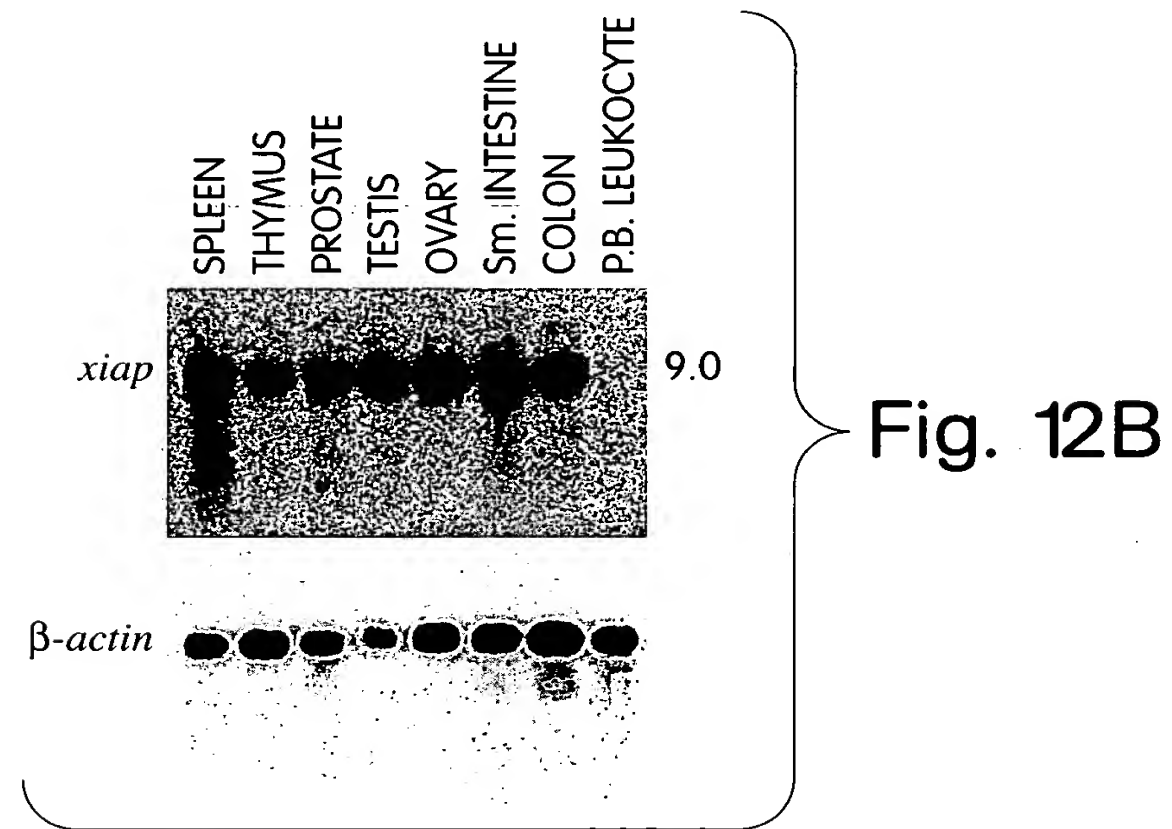
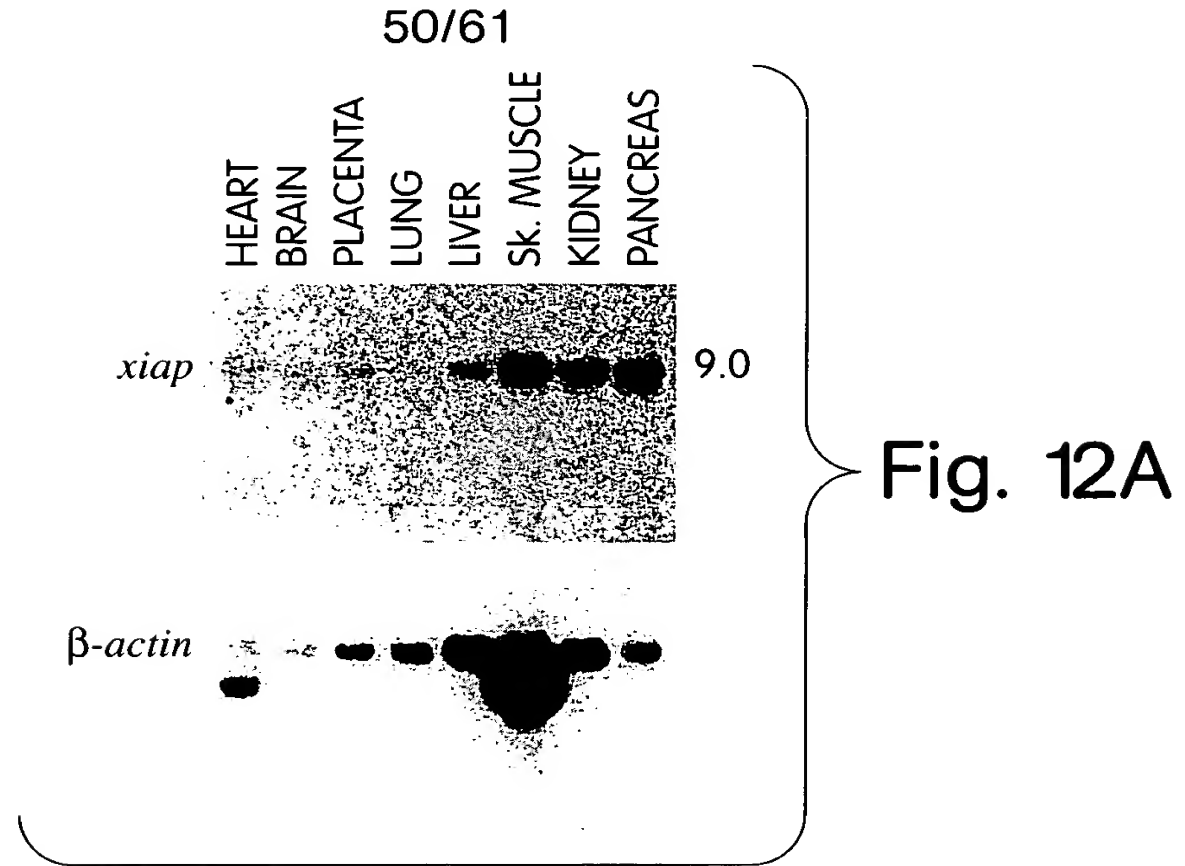
Alignment of RZF (Ring Zinc Finger) Domains

Baculovirus		Cydia pomonella	
Cp_iap		Orgyia pseudotsugata	
Op_iap		IAP on X chromosome	
Human		two different human IAP genes	
xiap		mouse homologue of human xiap gene	
hiap1, hiap2		Drosophila IAP gene, not clearly a homologue of xiap or hiap	
Mouse			
m-xiap			
Insect			
diap			
note on consensus:		The consensus line represents amino acids or very similar amino acids which are present in 6 of the 7 RZF sequences at each position. Capitalized residues are those that are in the consensus sequence.	
SEQ ID NO:32	hiap2	1	46
SEQ ID NO:33	hiap1	EqlrrlqEer	tCKVCMdkev sVvFiPCGHl vvCqeCApel rkCPiC
SEQ ID NO:34	m-xiap	EqlrrlpEer	tCKVCMdkev sIVFiPCGHl w CkdCApsl rkCPiC
SEQ ID NO:35	xiap	EqlrrlqEek	lSKICMdrni aIVFfPCGHl atCkqCAeav dkCPmC
SEQ ID NO:36	diap	EqlrrlqEek	lCKICMdrni aIVFvPCGHl vtCkqCAeav dkCPmC
SEQ ID NO:37	Cp_iap	EenrqlkDar	lCKVCLdeev gVvFlPCGHl atCnqCApev anCPmC
SEQ ID NO:38	Op_iap	EkepgveDsk	lCKICyveec iVcFvPCGHv vaCakCAIsv dkCPmC
SEQ ID NO:1	consensus	aveaevaDdr	lCKIClgack tVcFvPCGHv vaCgkCAagv ttCPvC
		E-----E--	-CKICM----- -V-F-PCGH- --C--CA--- --CP-C

Fig. 9







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INCUBATION: OVERNIGHT												
S: STANDARDS												
	Hg			CEM-CM ₃			GT/CEM			JKT		
HIV	-	-	+	-	-	+	-	-	+	-	-	+
PHA/PMA	-	+	-	-	+	-	-	+	-	-	+	-
S	+	-	-	+	-	-	+	-	-	+	-	-

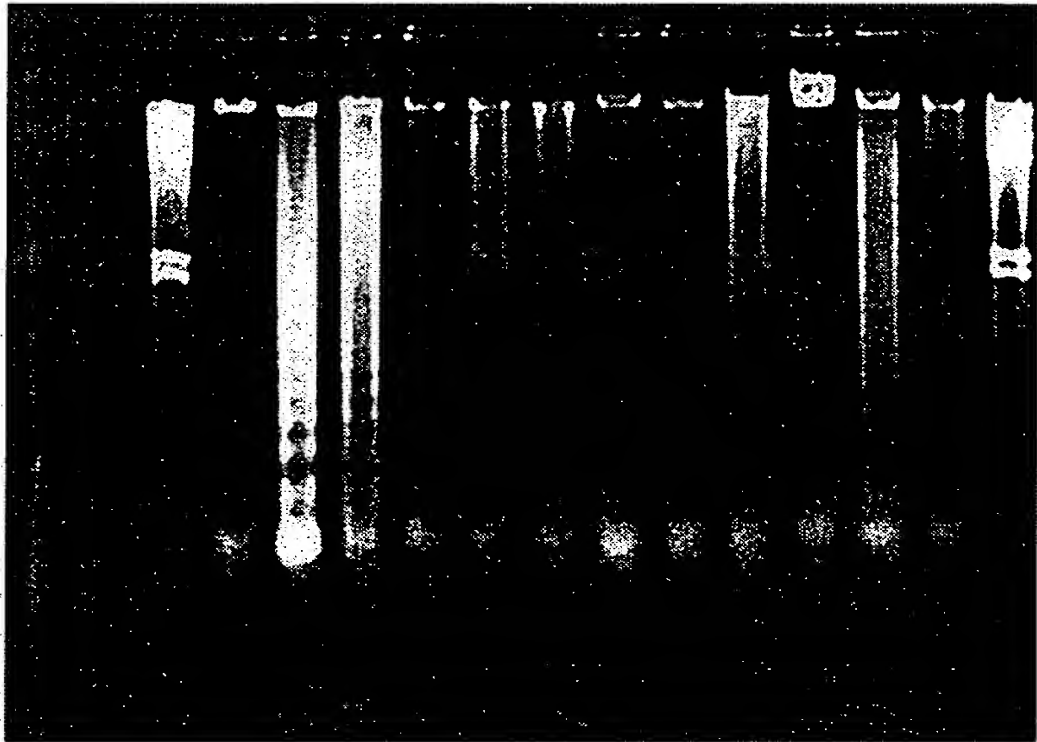


Fig. 13A

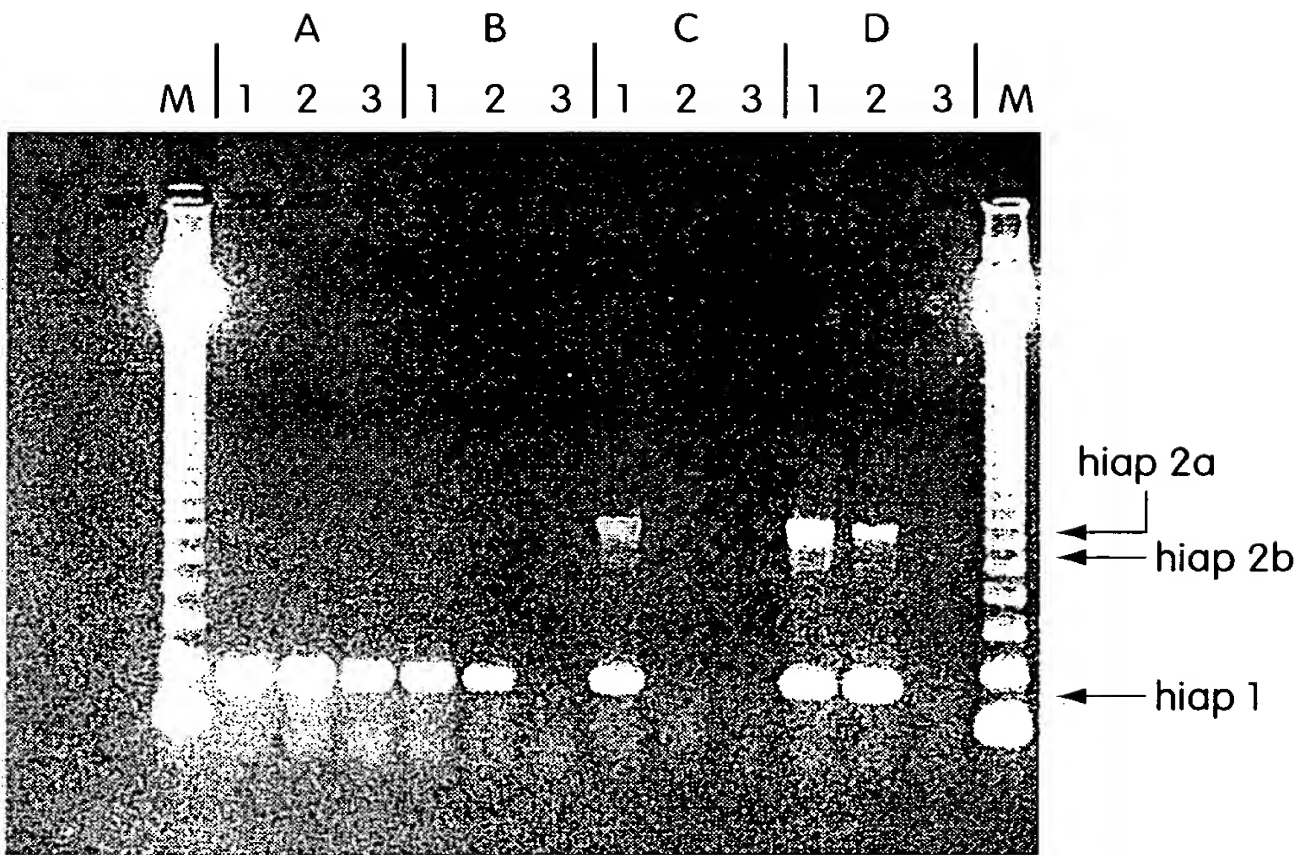


Fig. 13B

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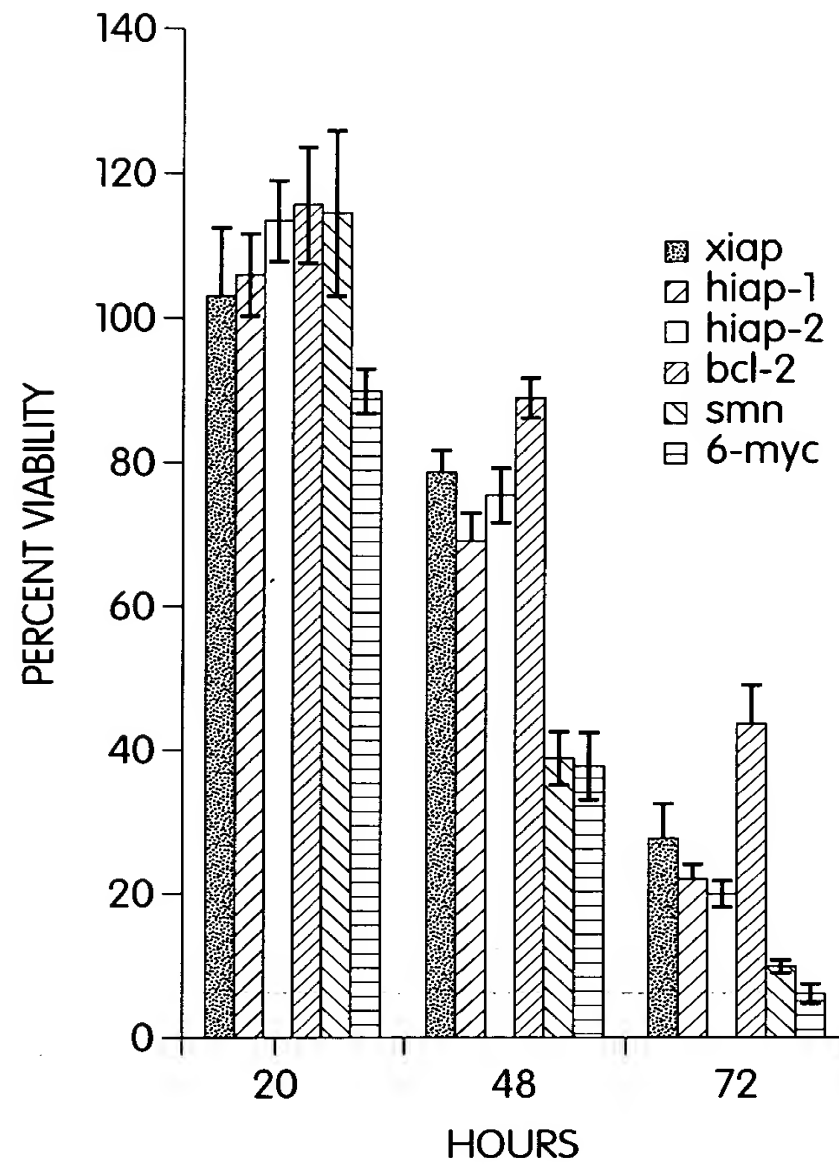


Fig. 14A

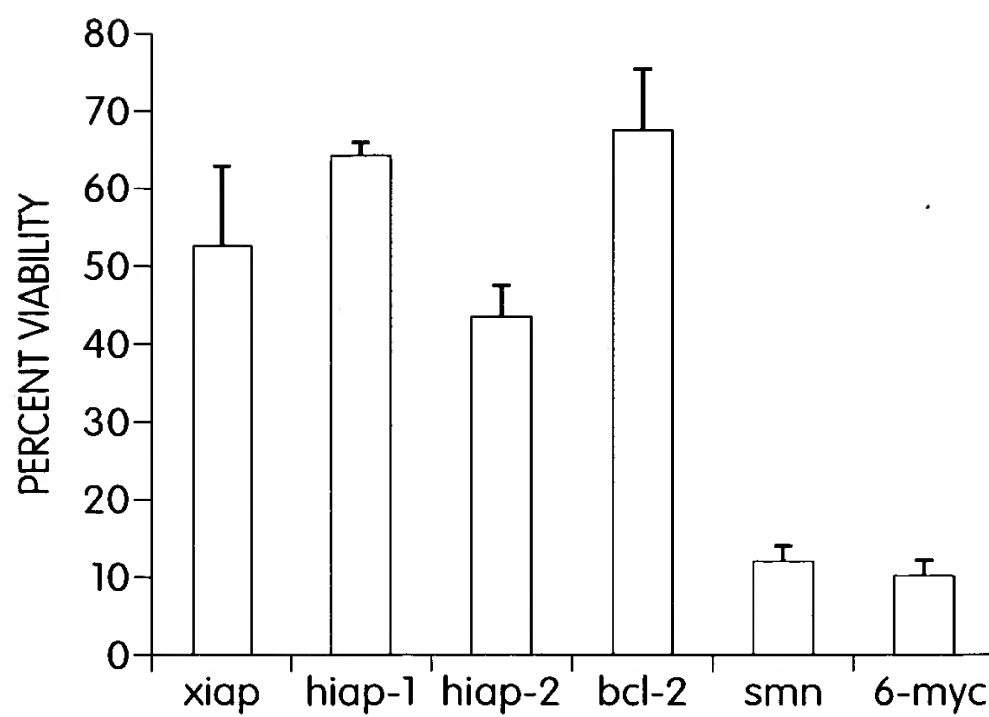


Fig. 14B

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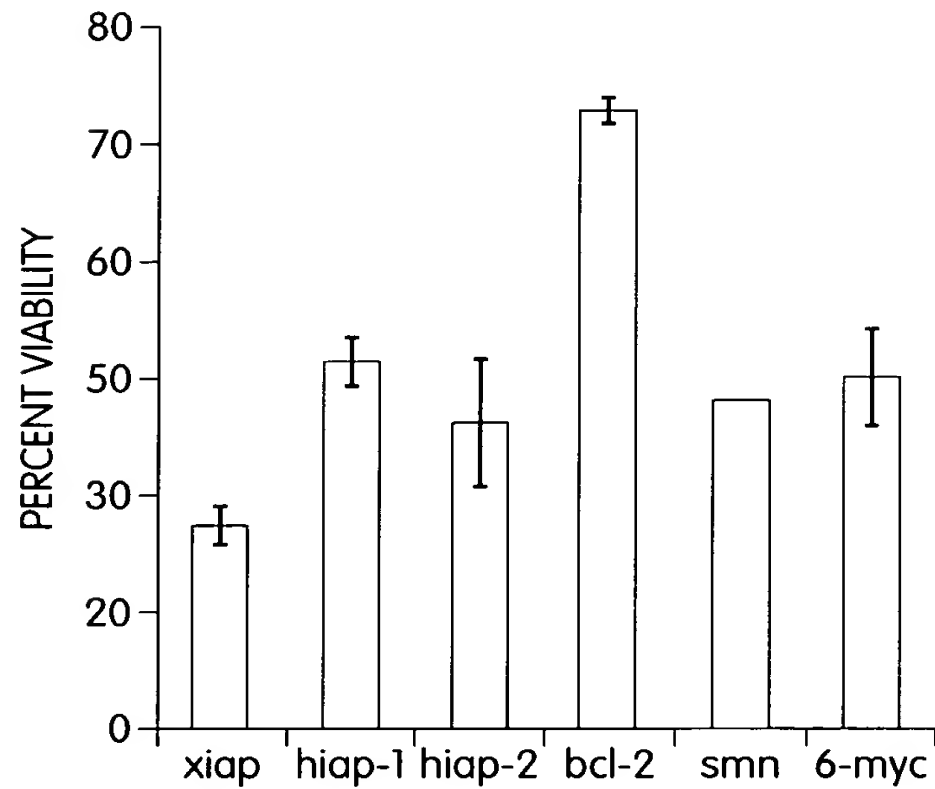


Fig. 14C

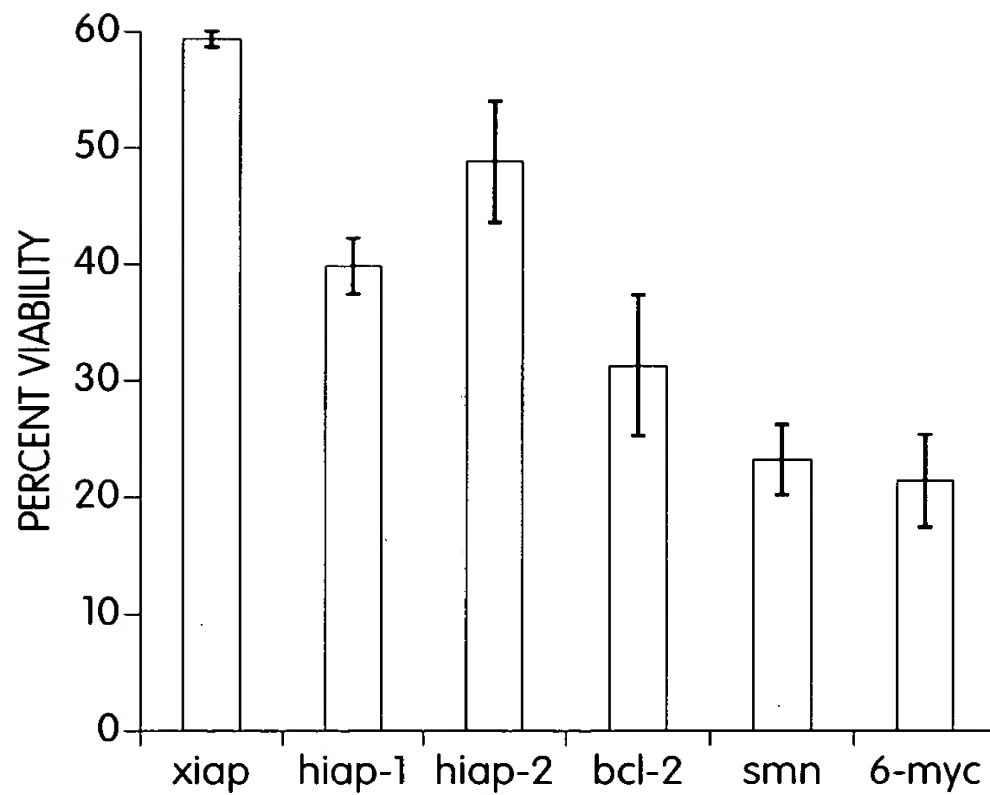


Fig. 14D

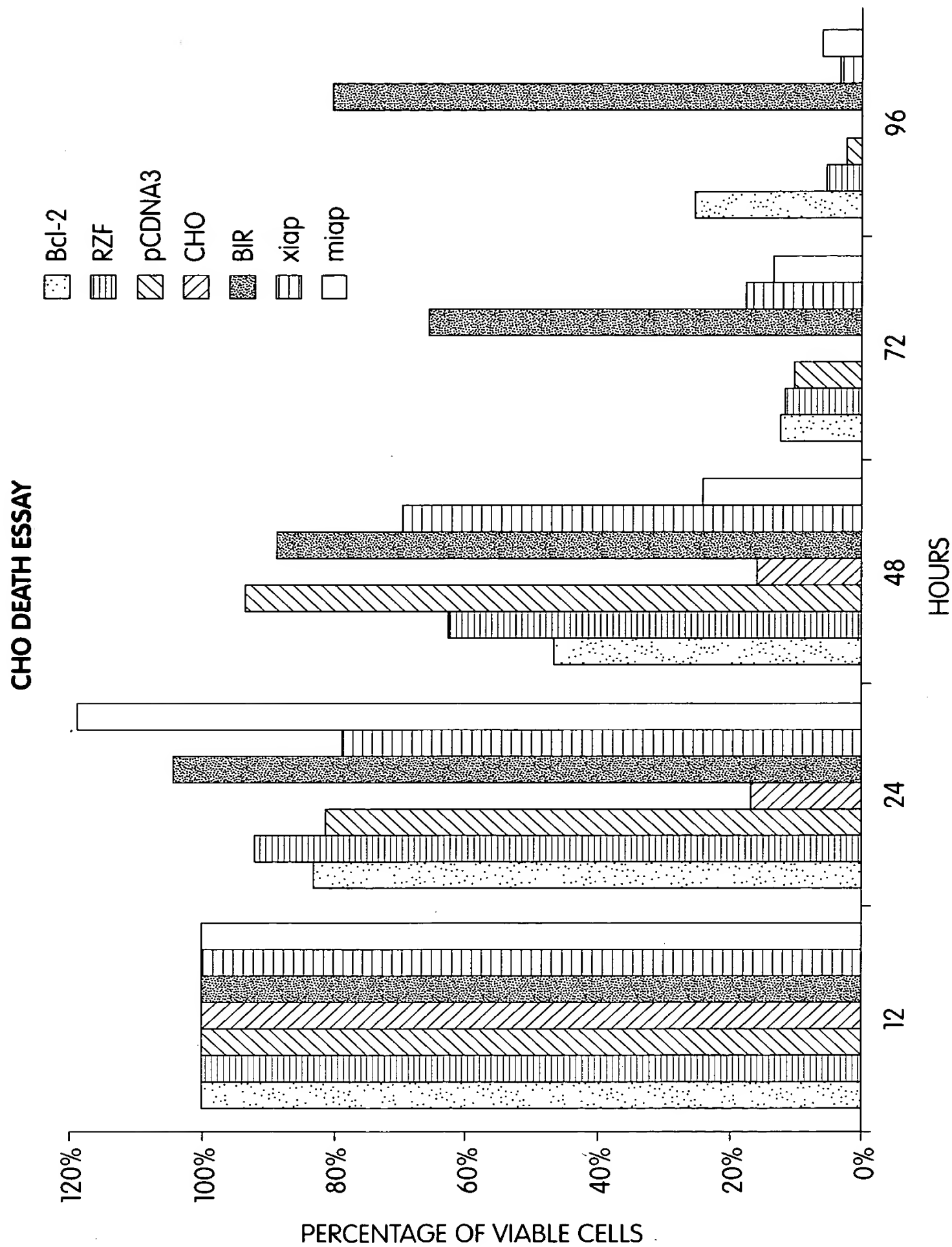


Fig. 15A

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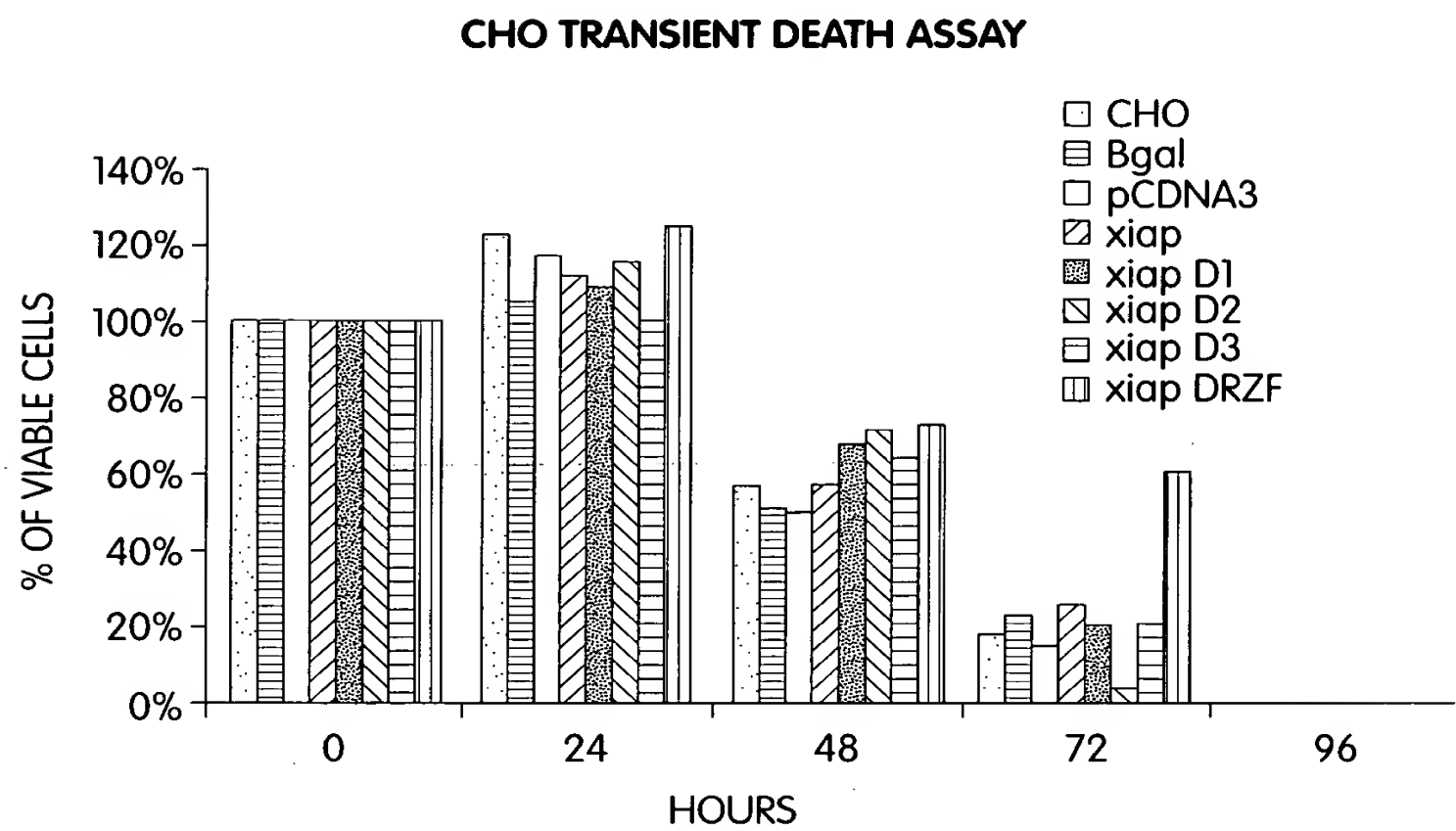


Fig. 15B

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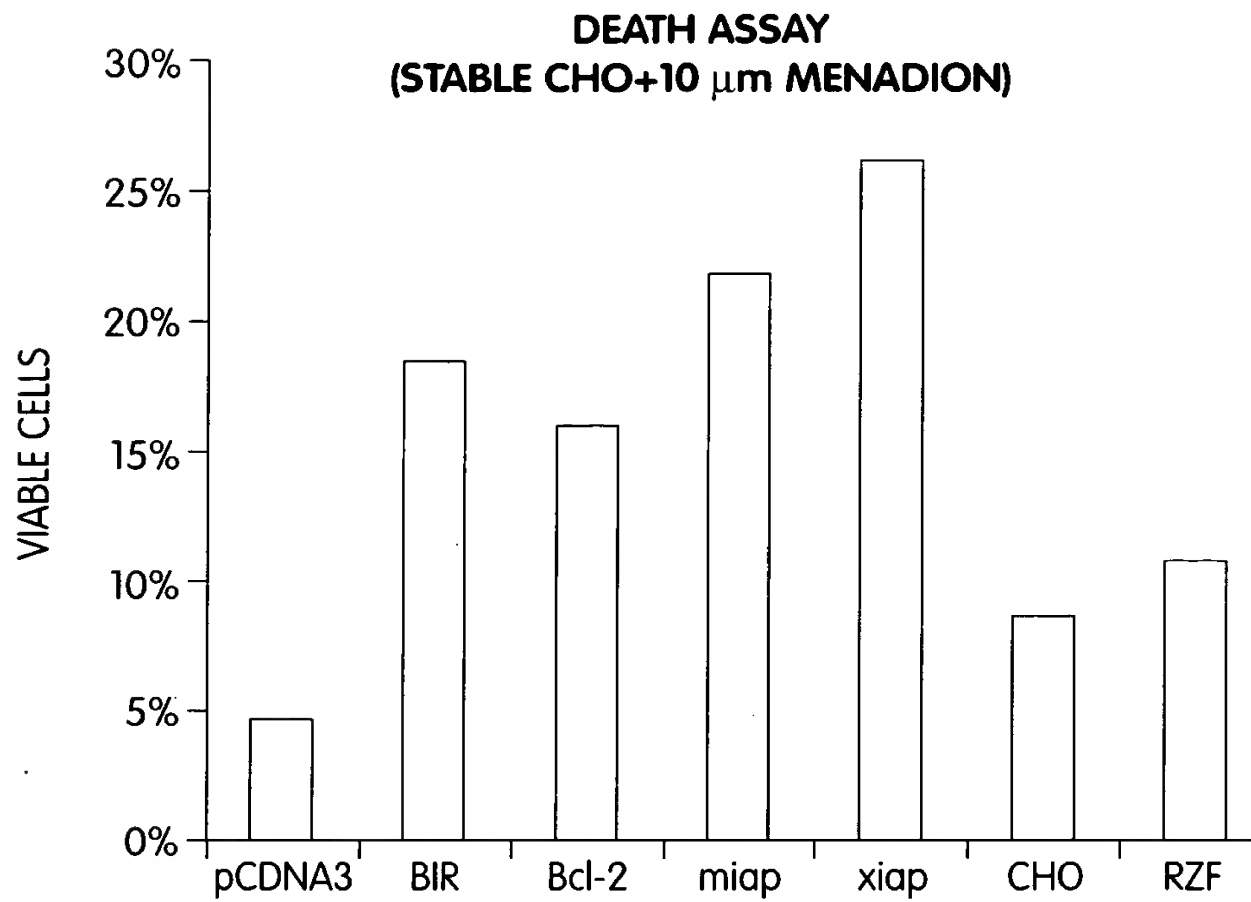


Fig. 16A

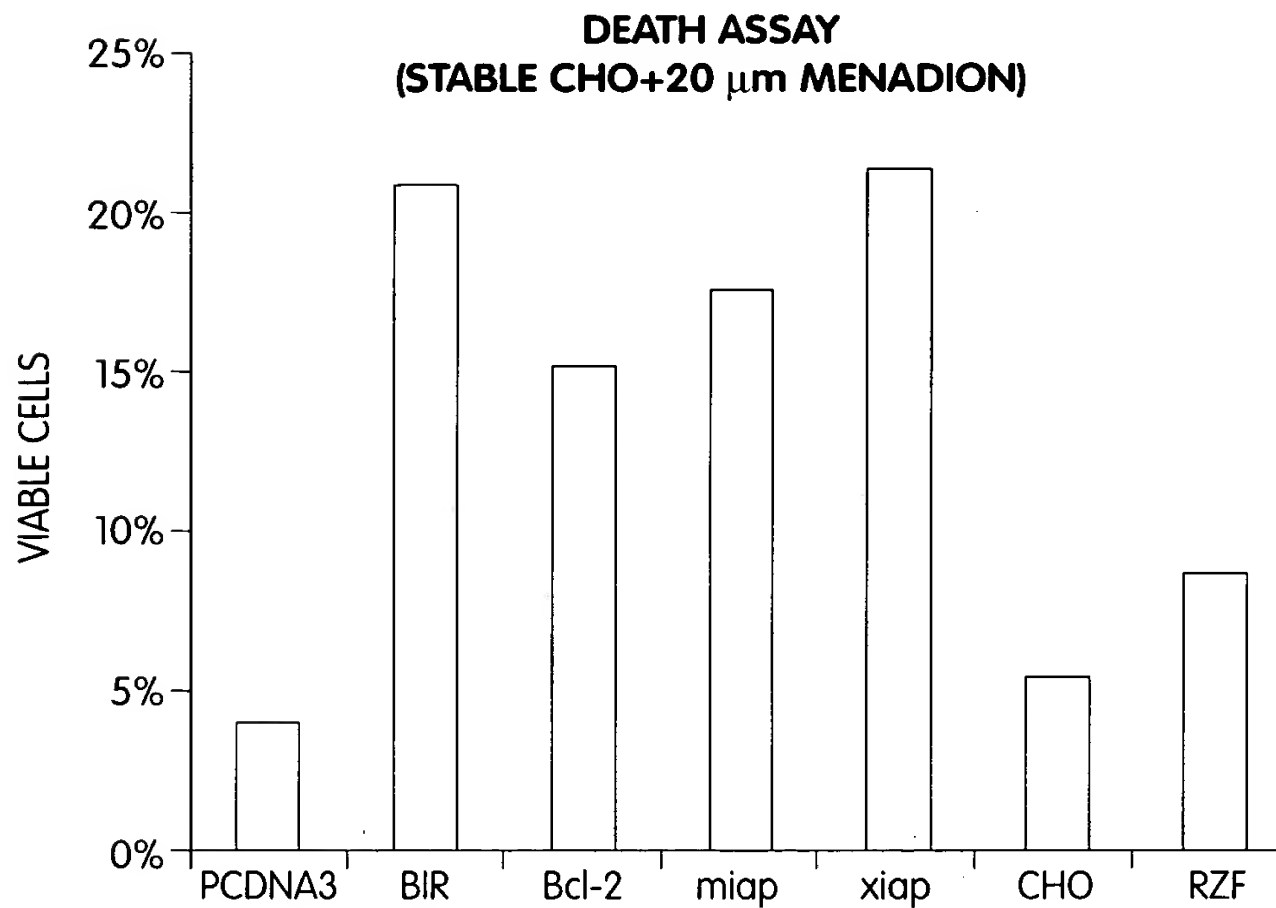


Fig. 16B

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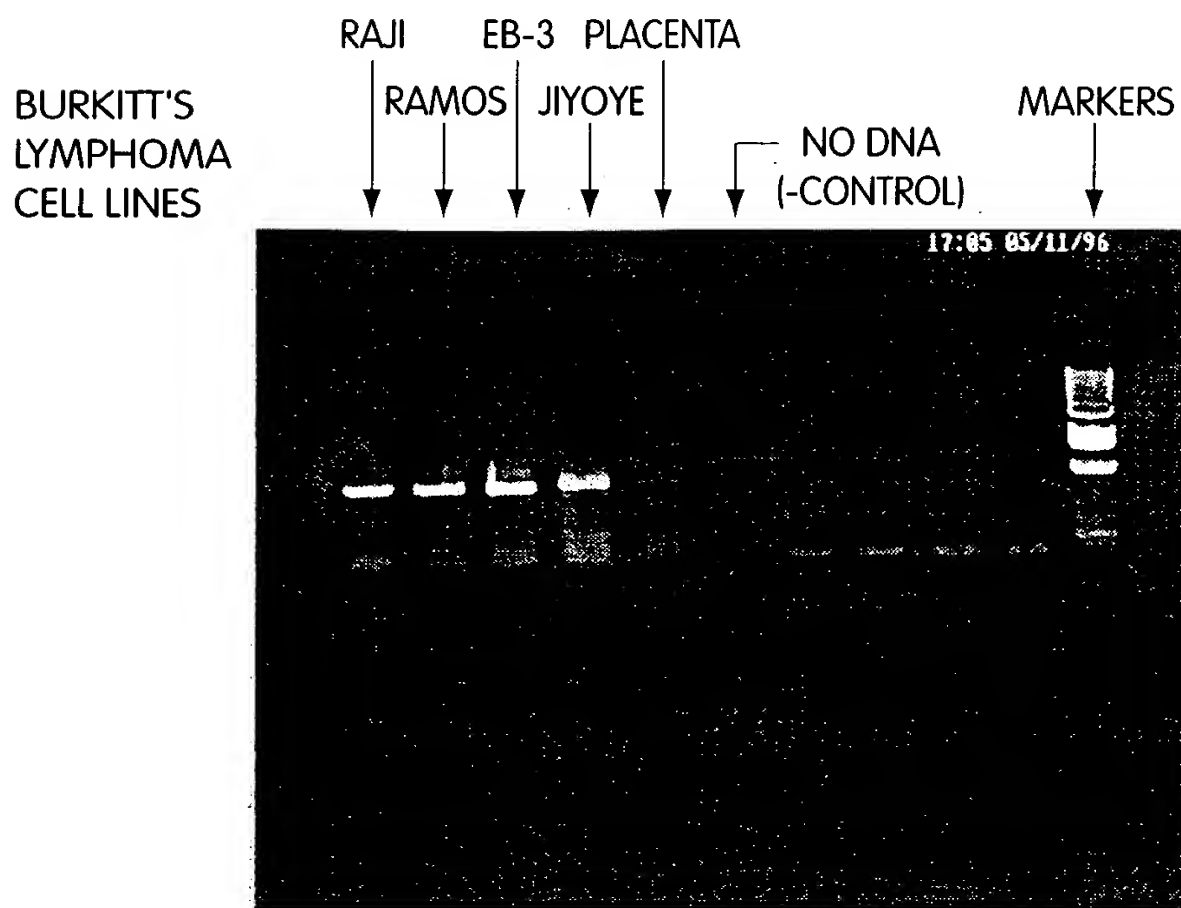


Fig. 17

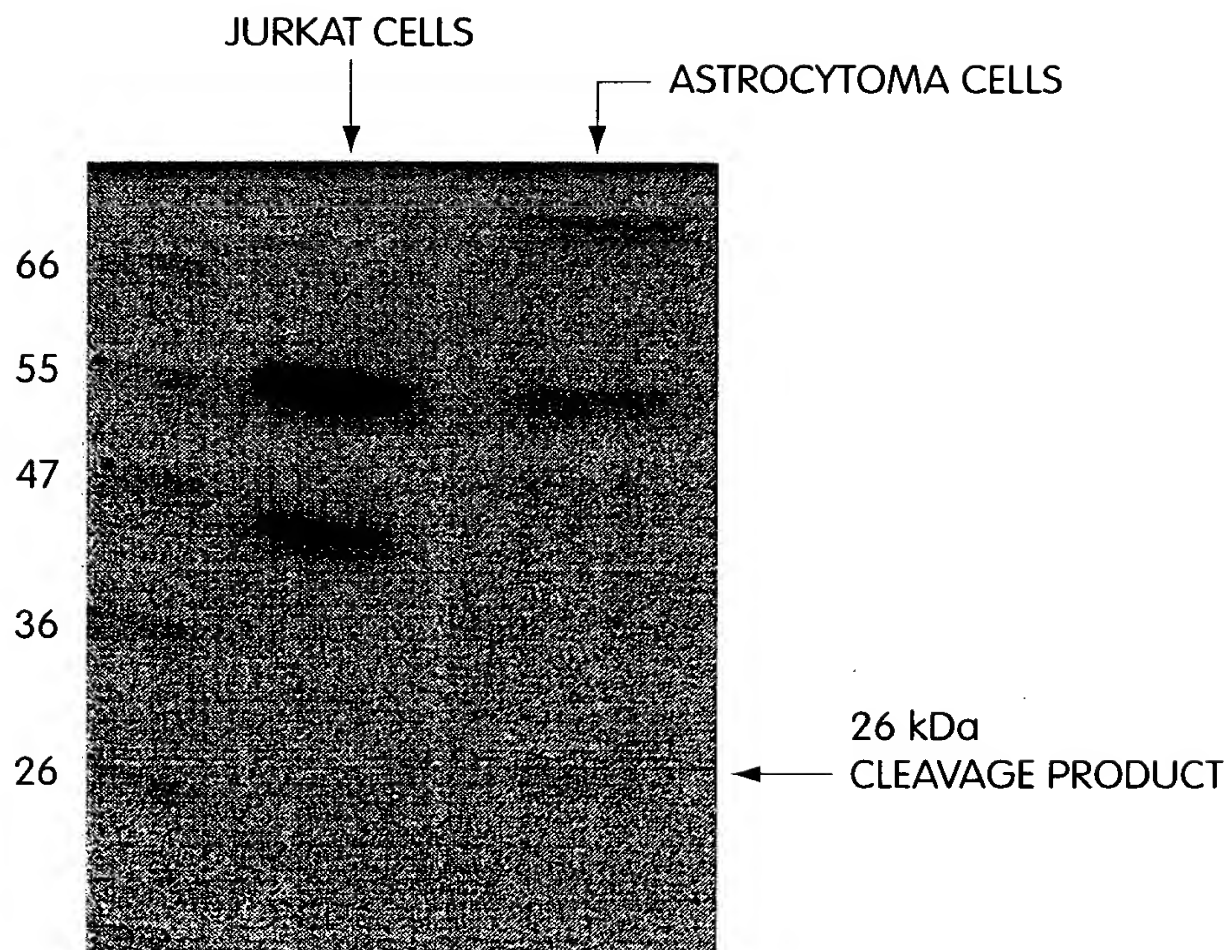


Fig. 18

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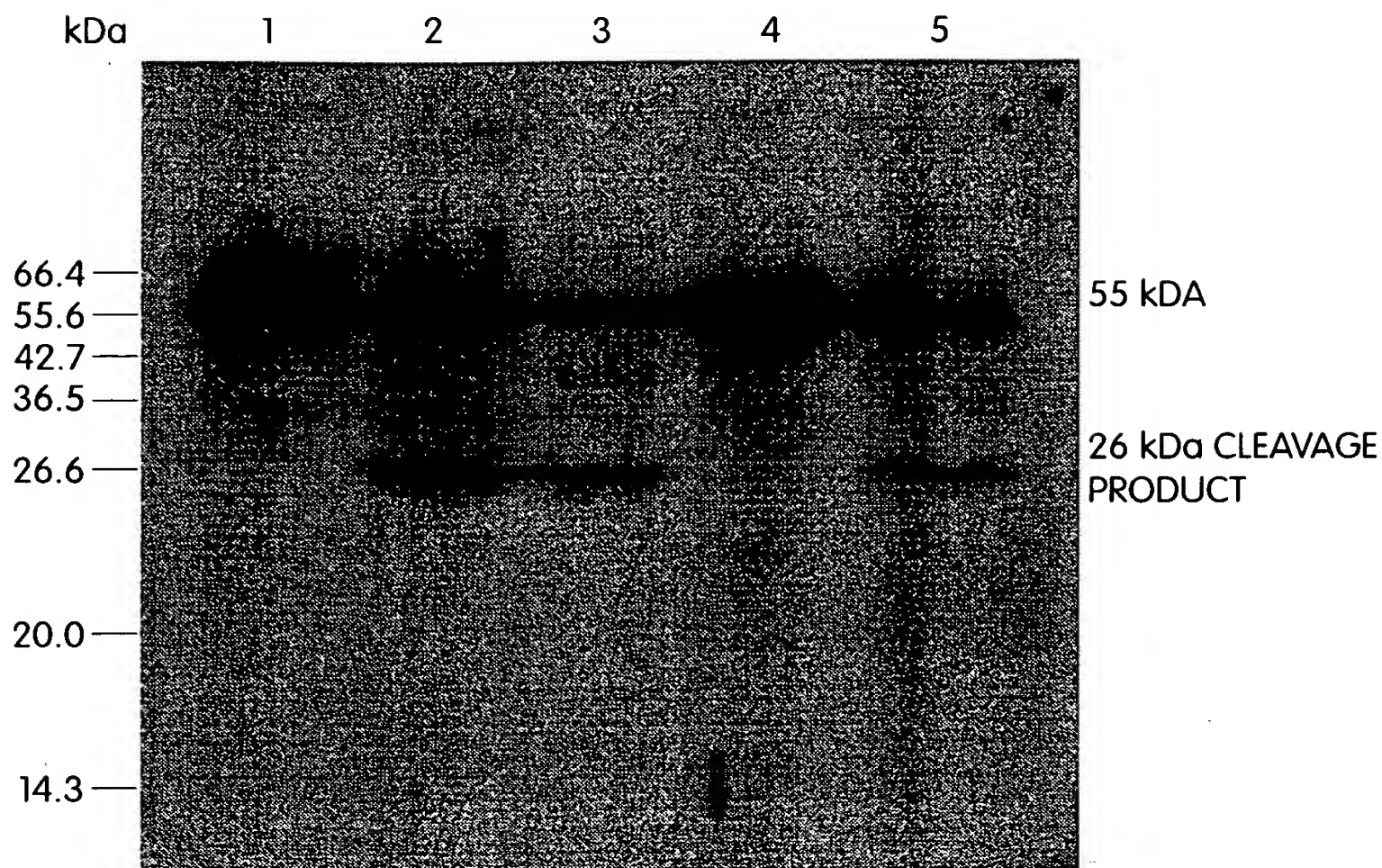


Fig. 19

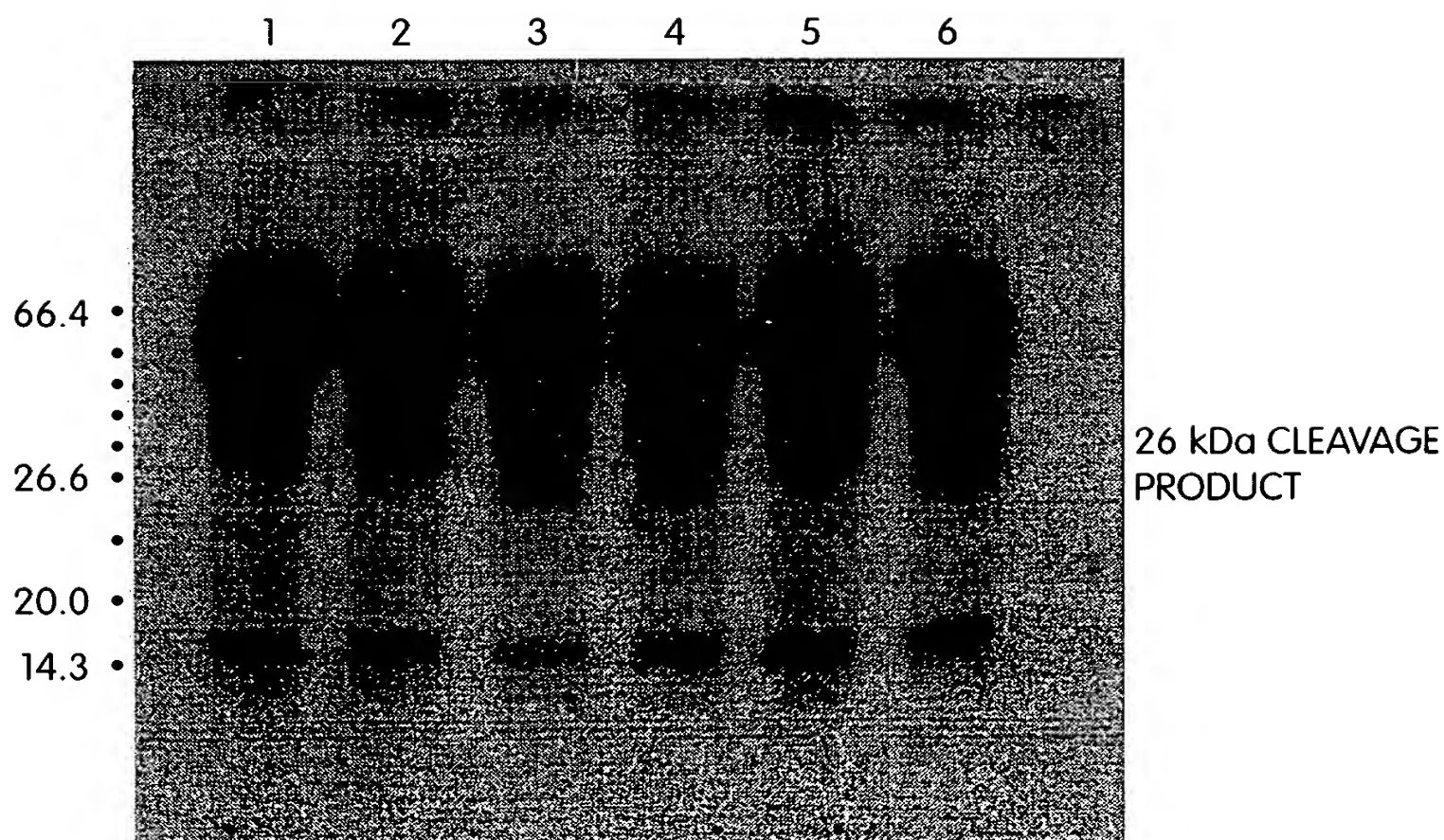


Fig. 20

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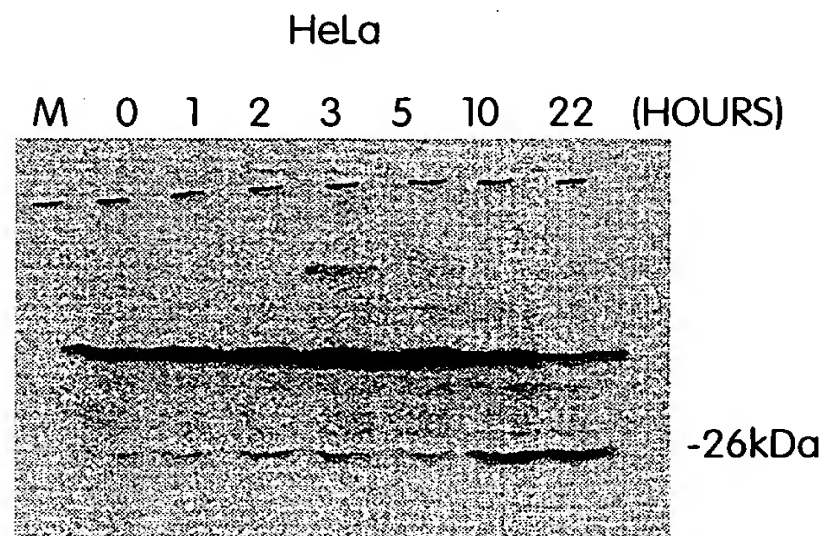


Fig. 21A

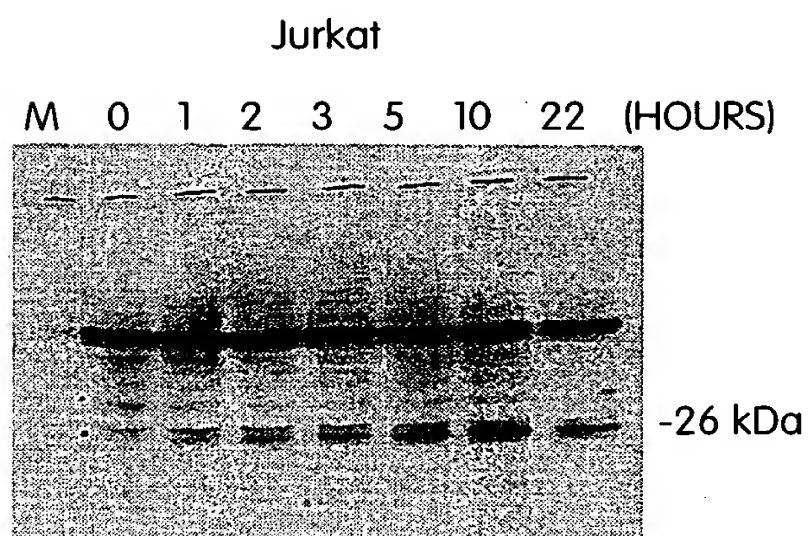


Fig. 21B

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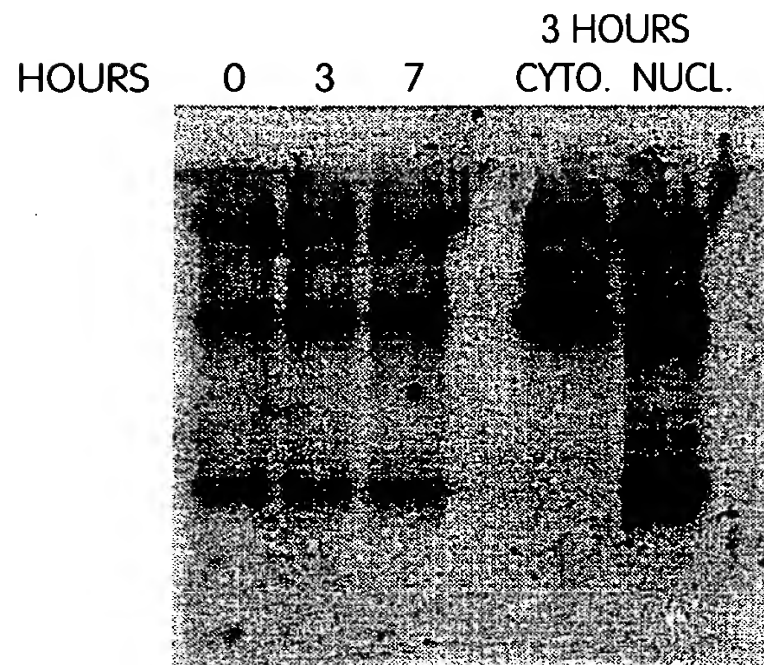


Fig. 22A

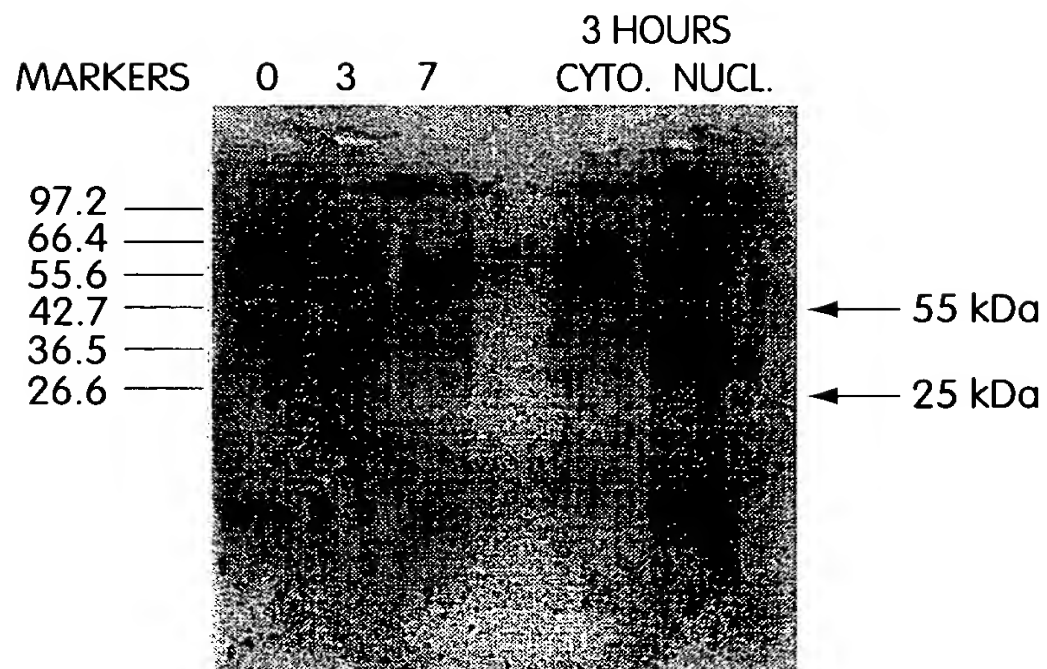


Fig. 22B

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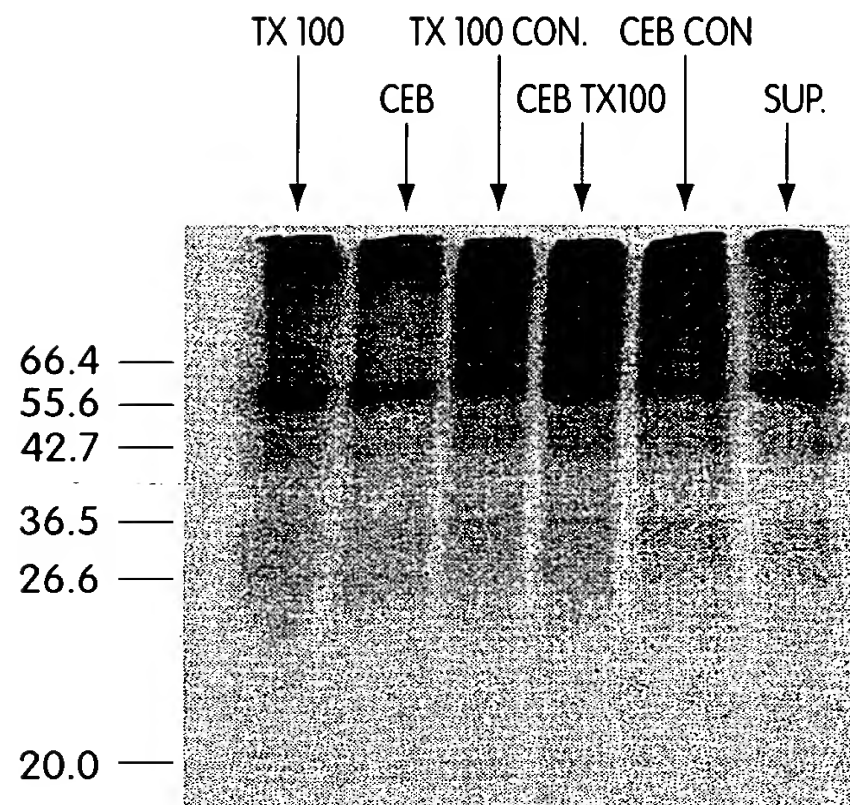


Fig. 23

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